SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Abrams, Mark A.
               Bauer, S. C.
               Braford-Goldberg, Sarah R.
               Caparon, Maire H.
               Easton, Alan M.
               Klein, Barbara K.
               McKearn, John P.
               Olins, Peter O.
               Paik, Kumnan
               Thomas, John W.

    (ii) TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

    (iii) NUMBER OF SEQUENCES: 197

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
            Corporate Patent Dept., Mail Zone O4E
        (B) STREET: 800 N. Lindbergh
        (C) CITY: St. Louis
        (D) STATE: Missouri
        (E) COUNTRY: USA
        (F) ZIP: 63167

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: not assigned
        (B) FILING DATE: 22-FEB-2002
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: 08/762,227
        (B) FILING DATE: 09-DEC-1996

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/192,325
        (B) FILING DATE: 14-FEB-1994

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/446,872
        (B) FILING DATE: 06-JUN-1995

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: S. Christopher Bauer
        (B) REGISTRATION NUMBER: 42,305
        (C) REFERENCE/DOCKET NUMBER: C-2790/6

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (636)737-6257

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 133 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 1
       (D) OTHER INFORMATION: /note= "Met- may or may not precede the
          amino acid in position 1"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 17
       (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser,
          Lys, Gly, Asp, Met, Gln, or Arg"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 18
       (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,
          His, Leu, Ile, Phe, Arg, or Gln"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 19
       (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met,
          Phe, Ile, Arg, Gly, Ala, or Cys"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 20
       (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile,
          Cys, Gln, Glu, Arg, Pro, or Ala"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 21
       (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp,
          Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser,
          or Val"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 22
       (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu,
          Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val,
          or Gly"

    (ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 23
       (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,

Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser, or
Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 24
    (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,
        Gly, Val, Arg, Ser, Phe, or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 25
    (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,
        His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 26
    (D) OTHER INFORMATION: /note= "Xaa at position 26 is His,
        Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 27
    (D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu,
        Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 28
    (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys,
        Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 29
    (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
        Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 30
    (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,
        His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 31
    (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,
        Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 32
    (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
        Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 33
    (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro,

Leu, Gln, Ala, Thr, or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 34
    (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
        Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe,
        Ile, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 35
    (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,
        Ala, Gly, Asn, Pro, Gln, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 36
    (D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp,
        Leu, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 37
    (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
        Ser, Pro, Trp, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 38
    (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 40
    (D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu,
        Trp, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 41
    (D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn,
        Cys, Arg, Leu, His, Met, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 42
    (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
        Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr,
        Ile, Met, or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 43
    (D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu,
        Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly,
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site

(B) LOCATION: 44
        (D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp,
              Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala,
              or Pro"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 45
        (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
              Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg,
              Ser, Ala, Ile, Glu, or His"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 46
        (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
              Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr,
              Ile, Val, or Gly"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 47
        (D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile,
              Gly, Val, Ser, Arg, Pro, or His"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 48
        (D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu,
              Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met,
              Val, or Asn"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 49
        (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,
              Arg, Ala, Gly, Pro, Asn, His, or Asp"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 50
        (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,
              Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His,
              Phe, Met, or Gln"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 51
        (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,
              Arg, Met, Pro, Ser, Thr, or His"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 52
        (D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn,
              His, Arg, Leu, Gly, Ser, or Thr"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 53
        (D) OTHER INFORMATION: /note= "Xaa at position 53 is

Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 54
    (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg,
        Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala,
        or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 55
    (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,
        Thr, Val, Ser, Leu, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 56
    (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,
        Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr,
        Phe, Leu, Val, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 57
    (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn
        or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 58
    (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu,
        Ser, Asp, Arg, Gln, Val, or Cys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 59
    (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu,
        Tyr, His, Leu, Pro, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 60
    (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala,
        Ser, Pro, Tyr, Asn, or Thr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 61
    (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe,
        Asn, Glu, Pro, Lys, Arg, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 62
    (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,
        His, Val, Arg, Pro, Thr, Asp, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 63

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(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg,
Tyr, Trp, Lys, Ser, His, Pro, or Val"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 64
   (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala,
Asn, Pro, Ser, or Lys"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 65
   (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val,
Thr, Pro, His, Leu, Phe, or Ser"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 66
   (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys,
Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 67
   (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,
Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 68
   (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
Val, Trp, Ser, Ile, Phe, Thr, or His"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 69
   (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 70
   (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn,
Leu, Val, Trp, Pro, or Ala"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 71
   (D) OTHER INFORMATION: /note= "Xaa at position 71 is
Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp,
or Asn"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 72
   (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,
Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:
   (A) NAME/KEY: Modified-site
   (B) LOCATION: 73

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(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala,
        Glu, Asp, Leu, Ser, Gly, Thr, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 74
        (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile,
                Met, Thr, Pro, Arg, Gly, or Ala"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 75
        (D) OTHER INFORMATION: /note= "Xaa at position 75 is
                Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln,
                or Leu"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 76
        (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
                Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 77
        (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile,
                Ser, Arg, Thr, or Leu"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 78
        (D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu,
                Ala, Ser, Glu, Phe, Gly, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 79
        (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Thr,
                Asn, Met, Arg, Ile, Gly, or Asp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 80
        (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
                Trp, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 81
        (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu,
                Gln, Gly, Ala, Trp, Arg, Val, or Lys"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 82
        (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
                Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala,
                Tyr, Phe, Ile, Met, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site

(B) LOCATION: 83
        (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro,
             Ala, Thr, Trp, Arg, or Met"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 84
        (D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys,
             Glu, Gly, Arg, Met, or Val"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 85
        (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu,
             Asn, Val, or Gln"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 86
        (D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro,
             Cys, Arg, Ala, or Lys"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 87
        (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu,
             Ser, Trp, or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 88
        (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala,
             Lys, Arg, Val, or Trp"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 89
        (D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr,
             Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 90
        (D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala,
             Pro, Ser, Thr, Gly, Asp, Ile, or Met"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 91
        (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala,
             Pro, Ser, Thr, Phe, Leu, Asp, or His"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 92
        (D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro,
             Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 93

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(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
Asp, Ser, Asn, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 94
(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 95
(D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala,
Trp, Phe, Ile, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 96
(D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro,
Lys, Tyr, Gly, Ile, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 97
(D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile,
Val, Lys, Ala, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 98
(D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met,
Val, Lys, Arg, Tyr, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 99
(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,
Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe,
or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 100
(D) OTHER INFORMATION: /note= "Xaa at position 100 is
Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 101
(D) OTHER INFORMATION: /note= "Xaa at position 101 is
Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser,
Ala, Gly, Ile, Leu, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 102
(D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly,
Leu, Glu, Lys, Ser, Tyr, or Pro"

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(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 103
    (D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp,
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 104
    (D) OTHER INFORMATION: /note= "Xaa at position 104 is
        Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala,
        Phe, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 105
    (D) OTHER INFORMATION: /note= "Xaa at position 105 is
        Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile,
        Asp, or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 106
    (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu,
        Ser, Ala, Lys, Thr, Ile, Gly, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 108
    (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg,
        Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 109
    (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
        Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 110
    (D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys,
        Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 111
    (D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu,
        Ile, Arg, Asp, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 112
    (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,
        Val, Gln, Tyr, Glu, His, Ser, or Phe"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 113
    (D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe,
        Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val,

or Asn"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 114
     (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr,
          Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 115
     (D) OTHER INFORMATION: /note= "Xaa at position 115 is
          Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or
          Met"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 116
     (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
          Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser,
          Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 117
     (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr,
          Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 118
     (D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu,
          Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 119
     (D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu,
          Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 120
     (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
          Ala, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 121
     (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala,
          Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 122
     (D) OTHER INFORMATION: /note= "Xaa at position 122 is
          Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr,
          or Cys"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site

12

```
            (B) LOCATION: 123
            (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala,
                    Met, Glu, His, Ser, Pro, Tyr, or Leu"


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

    Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
    1               5                   10                  15

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20                  25                  30

    Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                35                  40                  45

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                50                  55                  60

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    65                  70                  75                      80

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa
                100                 105                 110

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu
                115                 120                 125

    Ser Leu Ala Ile Phe
        130
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 133 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 1
        (D) OTHER INFORMATION: /note= "Met- may or may not precede
            the amino acid in position 1"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 17
        (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser,
            Gly, Asp, Met, or Gln"

  (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 18
        (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,
            His, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 19
    (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met
        or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 21
    (D) OTHER INFORMATION: /note="Xaa at position 21 is Asp
        or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 23
    (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,
        Ala, Leu, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 24
    (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,
        Val, or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 25
    (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,
        His, Gln, or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 26
    (D) OTHER INFORMATION: /note= "Xaa at position 26 is His
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 29
    (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
        Asn, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 30
    (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,
        Gly, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 31
    (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,
        Asp, Gly, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 32
    (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
        Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 33
    (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro
        or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 34
    (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
        Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe,
        Thr, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 35
    (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,
        Ala, Asn, Pro, Gln, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 37
    (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
        Ser, Pro, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 38
    (D) OTHER INFORMATION: /note="Xaa at position 38 is Asn
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 42
    (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
        Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr,
        or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 44
    (D) OTHER INFORMATON: /note="Xaa at position 44 is Asp
        or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 45
    (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
        Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 46
    (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
        Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile,
        Lys, Tyr, Val, or Cys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 50
    (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,
        Ala, Asn, Ser, or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 51
    (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,
        Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 54
    (D) OTHER INFORMATON: /note="Xaa at position 54 is Arg
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 55
    (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,
        Thr, Val, Leu, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 56
    (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,
        Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val,
        or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 60
    (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 62
    (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,
        Pro, Thr, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 63
    (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg
        or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 64
    (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala
        or Asn"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 65
    (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val
        or Thr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 66
    (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys
        or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 67
    (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser
        Phe or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 68
    (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
        Ile, Phe, or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 69
    (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
        Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 71
    (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,
        Pro, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 72
    (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,
        Glu, Arg, or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 73
    (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala
        or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 76
    (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
        Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 77
    (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile
        or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 79
    (D) OTHER INFORMATION: /note= "Xaa at position 79 is
        Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 80
    (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
        Gly, Glu, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 82
        (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
                Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile,
                Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 83
        (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro
                or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 85
        (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu
                or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 87
        (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu
                or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 88
        (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
                or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 91
        (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
                or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 93
        (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
                Asp, Ser, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 95
        (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
                Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 96
        (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro
                or Tyr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 97
        (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile
                or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 98
    (D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
        Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys,
        Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 99
    (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,
        Leu, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 100
    (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys,
        Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 101
    (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
        Pro, Met, Lys, Thr, His, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 104
    (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp
        or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 105
    (D) OTHER INFORMATION: /note= "Xaa at position 105 is
        Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile,
        Asp, or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 106
    (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu
        or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 108
    (D) OTHER INFORMATON: /note="Xaa at position 108 is Arg,
        Ala, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 109
    (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
        Thr, Glu, Leu, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 112
    (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,
        Val, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 114
    (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr
        or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 115
    (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 116
    (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
        Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 117
    (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 120
    (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
        Pro, Leu, His, Val, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 121
    (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala,
        Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 122
    (D) OTHER INFORMATION: /note= "Xaa at position 122 is
        Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr,
        or Cys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 123
    (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala,
        Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1               5                   10                  15

Xaa Xaa Xaa Ile Xaa Glu Xaa Xaa Xaa Xaa Leu Lys Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Asp Xaa Xaa Asn Leu Asn Xaa Glu Xaa Xaa Xaa Ile Leu
        35                  40                  45
```

20

```
Met Xaa Xaa Asn Leu Xaa Xaa Xaa Asn Leu Glu Xaa Phe Xaa Xaa Xaa
    50              55              60

Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ile Glu Xaa Xaa Leu Xaa Xaa
65              70              75              80

Leu Xaa Xaa Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Xaa
            85              90              95

Xaa Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Phe Xaa Xaa Lys Leu Xaa
            100             105             110

Phe Xaa Xaa Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu
    115             120             125

Ser Leu Ala Ile Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 133 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 1
        (D) OTHER INFORMATION: /note= "Met- may or may not precede
            the amino acid in position 1"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 17
        (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser,
            Gly, Asp, or Gln"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 18
        (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,
            His, or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 23
        (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,
            Ala, Leu, or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 25
        (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,
            His, or Gln"

    (ix) FEATURE:

(A) NAME/KEY: Modified-site
        (B) LOCATION: 26
        (D) OTHER INFORMATION: /note= "Xaa at position 26 is His
            or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 29
        (D) OTHER INFORMATION: /note="Xaa at position 29 is Gln
            or Asn"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 30
        (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro
            or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 32
        (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
            Arg, Asn, or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 34
        (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
            Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 35
        (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,
            Ala, Asn, or Pro"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 38
        (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn
            or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 42
        (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
            Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 45
        (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
            Val, Met, Leu, Ala, Asn, Glu, or Lys"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 46
        (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
            Phe, Ser, Gln, Glu, His, Val, or Thr"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site

22

(B) LOCATION: 50
                    (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,
                           Asn, Ser, or Asp"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 51
                    (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,
                           Arg, Pro, Thr, or His"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 55
                    (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,
                           Leu, or Gly"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 56
                    (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,
                           Gly, Ser, Ala, Asn, Val, Leu, or Gln"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 62
                    (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,
                           Pro, or Thr"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 64
                    (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala
                           or Asn"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 65
                    (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val
                           or Thr"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 67
                    (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser
                           or Phe"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 68
                    (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu
                           or Phe"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 69
                    (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
                           Ala, Glu, or Arg"

          (ix) FEATURE:
                    (A) NAME/KEY: Modified-site
                    (B) LOCATION: 76

(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
            Val, Asn, Pro, or Gly"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 77
        (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile
            or Leu"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 79
        (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,
            Asn, Met, Arg, Ile, or Gly"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 80
        (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
            Gly, Glu, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 82
        (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
            Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser,
            Thr, Tyr, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 87
        (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu
            or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 88
        (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
            or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 91
        (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
            or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 93
        (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
            Asp, or Ala"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 95
        (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
            Pro, Arg, Val, Gly, Asn, Ser, or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 98

```
                (D)  OTHER INFORMATION: /note= "Xaa at position 98 is His,
                     Ile, Asn, Ala, Thr, Gln, Glu, Lys, Met, Ser, Tyr,
                     Val, or Leu"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 99
                (D)  OTHER INFORMATION: /note= "Xaa at position 99 is Ile
                     or Leu"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 100
                (D)  OTHER INFORMATION: /note= "Xaa at position 100 is Lys
                     or Arg"

     (ix)  FEATURE;
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION:  101
                (D)  OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
                     Pro, Met, Lys, Thr, His, Asn, Ile, Leu, or Tyr"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 105
                (D)  OTHER INFORMATION: /note= "Xaa at position 105 is Asn,
                     Pro, Ser, Ile, or Asp"

     (ix)  FEATURE:
                (A)  NAME/KEY:  Modified-site
                (B)  LOCATION:  108
                (D)  OTHER INFORMATION:  /note= "Xaa at position 108 is Arg, Ala,
                     or Ser"
     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 109
                (D)  OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
                     Thr, Glu, Leu, or Ser"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 112
                (D)  OTHER INFORMATION: /note= "Xaa at position 112 is Thr
                     or Gln"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 116
                (D)  OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
                     Val, Trp, Ala, His, Phe, Tyr, or Ile"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 117
                (D)  OTHER INFORMATION: /note= "Xaa at position 117 is Thr
                     or Ser"

     (ix)  FEATURE:
                (A)  NAME/KEY: Modified-site
                (B)  LOCATION: 120
                (D)  OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
```

Pro, Leu, His, Val, or Gln"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION: 121
          (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala,
                Ser, Ile, Pro, or Asp"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION: 122
          (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln,
                Met, Trp, Phe, Pro, His, Ile, or Tyr"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION: 123
          (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala,
                Met, Glu, Ser, or Leu"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1               5                  10               15

Xaa Xaa Met Ile Asp Glu Xaa Ile Xaa Xaa Leu Lys Xaa Xaa Pro Xaa
            20                  25               30

Pro Xaa Xaa Asp Phe Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa Ile Leu
        35                  40               45

Met Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Glu Ala Phe Xaa Arg Xaa
    50                  55               60

Xaa Lys Xaa Xaa Xaa Asn Ala Ser Ala Ile Glu Xaa Xaa Leu Xaa Xaa
65                  70               75                   80

Leu Xaa Pro Cys Leu Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Pro
        85              90                   95

Ile Xaa Xaa Xaa Xaa Gly Asp Trp Xaa Glu Phe Xaa Xaa Lys Leu Xaa
        100             105              110

Phe Tyr Leu Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu
        115             120              125

Ser Leu Ala Ile Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 111 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 1
     (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may
         not precede the amino acid in position 1"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 3
     (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser,
         Lys, Gly, Asp, Met, Gln, or Arg"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 4
     (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn,
         His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 5
     (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met,
         Phe, Ile, Arg, Gly, Ala, or Cys"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 6
     (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile,
         Cys, Gln, Glu, Arg, Pro, or Ala"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 7
     (D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp,
         Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser,
         or Val"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 8
     (D) OTHER INFORMATION: /note= "Xaa at position 8 is Glu,
         Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val,
         or Gly"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 9
     (D) OTHER INFORMATION: /note= "Xaa at position 9 is
         Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser or Arg"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 10
     (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile,
         Gly, Val, Arg, Ser, Phe, or Leu"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 11
     (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,
         His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 12
    (D) OTHER INFORMATION: /note= "Xaa at position 12 is His,
        Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 13
    (D) OTHER INFORMATION: /note= "Xaa at position 13 is Leu,
        Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 14
    (D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys,
        Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 15
    (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,
        Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 16
    (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,
        His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 17
    (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro,
        Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 18
    (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
        Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 19
    (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro,
        Leu, Gln, Ala, Thr, or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 20
    (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,
        Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe,
        Ile, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 21
    (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,
        Ala, Gly, Asn, Pro, Gln, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 22
        (D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp,
                Leu, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 23
        (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
                Ser, Pro, Trp, or Ile"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 24
        (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
                or Ala"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 26
        (D) OTHER INFORMATION: /note= "Xaa at position 26 is Leu,
                Trp, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 27
        (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn,
                Cys, Arg, Leu, His, Met, or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 28
        (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
                Asp, Ser, Cys, Ala, Lys, Asn, Thr, Leu, Val, Glu,
                Phe, Tyr, Ile, or Met"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 29
        (D) OTHER INFORMATION: /note= "Xaa at position 29 is Glu,
                Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr,
                Gly, or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 30
        (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp,
                Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln,
                Ala, or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 31
        (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
                Pro, Phe, Val, Met, Leu, Thr, Lys, Asp, Asn, Arg,
                Ser, Ala, Ile, Glu, His, or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site

29

(B) LOCATION: 32
        (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
             Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala,
             Tyr, Ile, Val, or Gly"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 33
        (D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile,
             Gly, Val, Ser, Arg, Pro, or His"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 34
        (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
             Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala,
             Met, Val, or Asn"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 35
        (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met,
             Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 36
        (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,
             Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val,
             His, Phe, Met, or Gln"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 37
        (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
             Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 38
        (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,
             His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 39
        (D) OTHER INFORMATION: /note= "Xaa at position 39 is
             Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 40
        (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg,
             Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His,
             Ala, or Leu"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 41
        (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
             Thr, Val, Ser, Leu, or Gly"

30

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 42
    (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
        Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr,
        Phe, Leu, Val, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 43
    (D) OTHER INFORMATION: /note= "Xaa at position 43 is Asn
        or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 44
    (D) OTHER INFORMATION: /note= "Xaa at position 44 is Leu,
        Ser, Asp, Arg, Gln, Val, or Cys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 45
    (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu,
        Tyr, His, Leu, Pro, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 46
    (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala,
        Ser, Pro, Tyr, Asn, or Thr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 47
    (D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe,
        Asn, Glu, Pro, Lys, Arg, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 48
    (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
        His, Val, Arg, Pro, Thr, Asp, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 49
    (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg,
        Tyr, Trp, Lys, Ser, His, Pro, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 50
    (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala,
        Asn, Pro, Ser, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 51
    (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val,
        Thr, Pro, His, Leu, Phe, or Ser"

31

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 52
        (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys,
             Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 53
        (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
             Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 54
        (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,
             Val, Trp, Ser, Ile, Phe, Thr, or His"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 55
        (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
             Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 56
        (D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn,
             Leu, Val, Trp, Pro, or Ala"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 57
        (D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
             Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 58
        (D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
             Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 59
        (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala,
             Glu, Asp, Leu, Ser, Gly, Thr, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 60
        (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile,
             Met, Thr, Pro, Arg, Gly, Ala"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 61
        (D) OTHER INFORMATION: /note= "Xaa at position 61 is
             Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln,
             or Leu"

32

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(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 62
       (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
            Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 63
       (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile,
            Ser, Arg, Thr, or Leu"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 64
       (D) OTHER INFORMATION: /note= "Xaa at position 64 is Leu,
            Ala, Ser, Glu, Phe, Gly, or Arg"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 65
       (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
            Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 66
       (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,
            Trp, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 67
       (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,
            Gln, Gly, Ala, Trp, Arg, Val, or Lys"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 68
       (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
            Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala,
            Tyr, Phe, Ile, Met, or Val"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 69
       (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro,
            Ala, Thr, Trp, Arg, or Met"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 70
       (D) OTHER INFORMATION: /note= "Xaa at position 70 is Cys,
            Glu, Gly, Arg, Met, or Val"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION: 71
       (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu,
            Asn, Val, or Gln"
```

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 72
    (D) OTHER INFORMATION: /note= "Xaa at position 72 is Pro,
        Cys, Arg, Ala, or Lys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 73
    (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu,
        Ser, Trp, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 74
    (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala,
        Lys, Arg, Val, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 75
    (D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr,
        Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 76
    (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala,
        Pro, Ser, Thr, Gly, Asp, Ile, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 77
    (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala,
        Pro, Ser, Thr, Phe, Leu, Asp, or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 78
    (D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro,
        Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 79
    (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,
        Asp, Ser, Asn, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 80
    (D) OTHER INFORMATION: /note= "Xaa at position 80 is Arg,
        Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 81
    (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,
        Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser,
        Ala, Trp, Phe, Ile, or Tyr"

```
(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 82
      (D)  OTHER INFORMATION: /note= "Xaa at position 82 is Pro,
                 Lys, Tyr, Gly, Ile, or Thr"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 83
      (D)  OTHER INFORMATION: /note= "Xaa at position 83 is Ile,
                 Val, Lys, Ala, or Asn"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 84
      (D)  OTHER INFORMATION: /note= "Xaa at position 84 is His,
                 Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser,
                 Phe, Met, Val, Lys, Arg, Tyr, or Pro"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 85
      (D)  OTHER INFORMATION: /note= "Xaa at position 85 is
                 Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser,
                 Phe, or His"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 86
      (D)  OTHER INFORMATION: /note= "Xaa at position 86 is
                 Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 87
      (D)  OTHER INFORMATION: /note= "Xaa at position 87 is
                 Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn,
                 Ser, Ala, Gly, Ile, Leu, or Gln"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 88
      (D)  OTHER INFORMATION: /note= "Xaa at position 88 Gly,
                 Leu, Glu, Lys, Ser, Tyr, or Pro"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 89
      (D)  OTHER INFORMATION: /note= "Xaa at position 89 is Asp
                 or Ser"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
      (B)  LOCATION: 90
      (D)  OTHER INFORMATION: /note= "Xaa at position 90 is
                 Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys,
                 Ala, Phe, or Gly"

(ix)  FEATURE:
      (A)  NAME/KEY: Modified-site
```

(B) LOCATION: 91
            (D) OTHER INFORMATION: /note= "Xaa at position 91 is
                 Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys,
                 Ile, Asp, or His"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 92
            (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu,
                 Ser, Ala, Lys, Thr, Ile, Gly, or Pro"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 94
            (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
                 Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 95
            (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
                 Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 96
            (D) OTHER INFORMATION: /note= "Xaa at position 96 is Lys,
                 Asn, Thr, Leu, Gln, Arg, His, Glu, Ser, Ala,
                 or Trp"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 97
            (D) OTHER INFORMATION: /note= "Xaa at position 97 is Leu,
                 Ile, Arg, Asp, or Met"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 98
            (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,
                 Val, Gln, Tyr, Glu, His, Ser, or Phe"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 99
            (D) OTHER INFORMATION: /note= "Xaa at position 99 is Phe,
                 Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile,
                 Val, or Asn"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 100
            (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr,
                 Cys, His, Ser, Trp, Arg, or Leu"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 101
            (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu,
                 Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 102
    (D) OTHER INFORMATION: /note= "Xaa at position 102 is
        Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp,
        Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 103
    (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,
        Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 104
    (D) OTHER INFORMATION: /note= "Xaa at position 104 is Leu,
        Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 105
    (D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu,
        Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 106
    (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
        Ala, Pro, Leu, His, Val or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 107
    (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,
        Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 108
    (D) OTHER INFORMATION: /note= "Xaa at position 108 is
        Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr,
        or Cys"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 109
    (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,
        Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      35   40   45

37

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa
                85                  90                  95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln
                100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 1
        (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may
            not precede the amino acid in position 1"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 3
        (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser,
            Gly, Asp, Met, or Gln"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 4
        (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn,
            His, or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 5
        (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met
            or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 7
        (C) OTHER INFORMATON: /note= "Xaa at position 7 is Asp or Glu"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 9
        (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile,
            Ala, Leu, or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile,
                     Val, or Leu"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 11
                 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,
                     His, Gln, or Ala"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 12
                 (D) OTHER INFORMATION: /note= "Xaa at position 12 is His
                     or Ala"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 15
                 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,
                     Asn, or Val"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 16
                 (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,
                     Gly, or Gln"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 17
                 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro,
                     Asp, Gly, or Gln"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 18
                 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
                     Arg, Gln, Asn, Gly, Ala, or Glu"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 19
                 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro
                     or Glu"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 20
                 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,
                     Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe,
                     Thr, or Met"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 21
                 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,
                     Ala, Asn, Pro, Gln, or Val"

     (ix) FEATURE:
                 (A) NAME/KEY: Modified-site
                 (B) LOCATION: 23

(D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
            Ser, Pro, or Trp"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 24
        (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
            or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 28
        (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
            Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 30
        (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp
            or Glu"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 31
        (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
            Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 32
        (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
            Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys,
            Tyr, Val, or Cys"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 36
        (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,
            Ala, Asn, Ser, or Asp"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 37
        (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
            Arg, Met, Pro, Ser, Thr, or His"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 40
        (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg
            or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 41
        (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
            Thr, Val, Leu, or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 42

(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
                  Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val,
                  or Lys"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 46
             (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala
                  or Ser"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 48
             (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
                  Pro, Thr, or Ile"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 49
             (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg
                  or Lys"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 50
             (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala
                  or Asn"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 51
             (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
                  or Thr"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 52
             (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys
                  or Arg"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 53
             (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
                  Phe, or His"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 54
             (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,
                  Ile, Phe, or His"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 55
             (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
                  Ala, Pro, Thr, Glu, Arg, or Gly"

     (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 57

5   (D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
                Pro, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 58
    (D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
           Glu, Arg, or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 59
    (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala
           or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 62
    (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
           Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 63
    (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile
           or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 65
    (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
           Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 66
    (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,
           Gly, Glu, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 68
    (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
           Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met,
           Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 69
    (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro
           or Thr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 71
    (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu
           or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu
            or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 74
        (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala
            or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 77
        (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala
            or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 79
        (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,
            Asp, Ser, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 81
        (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,
            Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 82
        (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro
            or Tyr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 83
        (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile
            or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 84
        (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,
            Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys,
            Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 85
        (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile,
            Leu, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 86
        (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys,
            Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 87

(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,
            Pro, Met, Lys, His, Thr, Asn, Ile, Leu, or Tyr"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 90
        (D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp
            or Leu"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 91
        (D) OTHER INFORMATION: /note="Xaa at position 91 is Asn,
            Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp,
            or His"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 92
        (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu
            or Gly"

    (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 94
         (C) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
             Ala, or Ser"
   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 95
        (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
            Thr, Glu, Leu, or Ser"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 98
        (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,
            Val, or Gln"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 100
        (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr
            or Trp"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 101
        (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu
            or Ala"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 102
        (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,
            Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

   (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 103
        (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr

or Ser"

        (ix) FEATURE:
              (A) NAME/KEY: Modified-site
              (B) LOCATION: 106
              (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
                    Pro, Leu, His, Val, or Gln"

        (ix) FEATURE:
              (A) NAME/KEY: Modified-site
              (B) LOCATION: 107
              (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,
                    Ser, Ile, Asn, Pro, Asp, or Gly"

        (ix) FEATURE:
              (A) NAME/KEY: Modified-site
              (B) LOCATION: 108
              (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln,
                    Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

        (ix) FEATURE:
              (A) NAME/KEY: Modified-site
              (B) LOCATION: 109
              (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,
                    Met, Glu, His, Ser, Pro, Tyr, or Leu"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

    Asn Cys Xaa Xaa Xaa Ile Xaa Glu Xaa Xaa Xaa Xaa Leu Lys Xaa Xaa
    1   5   10   15

    Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Asn Leu Asn Xaa Glu Xaa Xaa Xaa
            20   25   30

    Ile Leu Met Xaa Xaa Asn Leu Xaa Xaa Xaa Asn Leu Glu Xaa Phe Xaa
            35   40   45

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ile Glu Xaa Xaa Leu
        50   55   60

    Xaa Xaa Leu Xaa Xaa Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg
    65   70   75   80

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Phe Xaa Xaa Lys
                85   90   95

    Leu Xaa Phe Xaa Xaa Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln
                100   105   110

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 111 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: peptide

        (ix) FEATURE:

                              45

(A) NAME/KEY: Modified-site
        (B) LOCATION: 1
        (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may
            not precede the amino acid in position 1"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 3
        (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser,
            Gly, Asp, or Gln"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 4
        (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn,
            His, or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 9
        (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile,
            Ala, Leu, or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 11
        (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,
            His, or Gln"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 12
        (D) OTHER INFORMATION: /note= "Xaa at position 12 is His
            or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 15
        (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln
            or Asn"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 16
        (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro
            or Gly"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 18
        (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
            Arg, Asn, or Ala"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 20
        (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,
            Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site

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(B) LOCATION: 21
            (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,
                   Ala, Asn, or Pro"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 24
            (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
                   or Ala"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 28
            (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
                   Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 31
            (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
                   Val, Met, Leu, Ala, Asn, Glu, or Lys"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 32
            (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
                   Phe, Ser, Ala, Gln, Glu, His, Val, or Thr"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 36
            (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,
                   Asn, Ser, or Asp"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 37
            (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
                   Arg, Pro, Thr, or His"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 41
            (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
                   Leu, or Gly"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 42
            (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
                   Gly, Ser, Ala, Asn, Val, Leu, or Gln"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 48
            (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
                   Pro, or Thr"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 50

(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala
or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 53
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser
or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 54
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu
or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
Ala, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 62
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
Val, Asn, Pro, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 63
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile
or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
Asn, Met, Arg, Ile, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 66
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,
Gly, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 68
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser,
Thr, Tyr, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu
            or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 74
        (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala
            or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 77
        (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala
            or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 79
        (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,
            Asp, or Ala"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 81
        (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,
            Pro, Arg, Val, Gly, Asn, Ser, or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 84
        (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,
            Ile, Asn, Leu, Ala, Thr, Arg, Gln, Glu, Lys, Met,
            Ser, Tyr, or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 85
        (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile
            or Leu"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 86
        (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys
            or Arg"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 87
        (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,
            Pro, Met, Lys, His, Pro, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 91
        (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn,
            Pro, Ser, Ile, or Asp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 94

(D) OTHER INFORMATION: /note="Xaa at position 94 is Arg,
               Ala, or Ser"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 95
         (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
               Thr, Glu, Leu, or Ser"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 98
         (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr
               or Gln"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 102
         (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,
               Val, Trp, or Ile"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 103
         (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,
               Ala, His, Phe, Tyr, or Ser"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 106
         (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
               Pro, Leu, His, Val, or Gln"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 107
         (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,
               Ser, Ile, Pro, or Asp"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 108
         (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln,
               Met, Trp, Phe, Pro, His, Ile, or Tyr"

  (ix) FEATURE:
         (A) NAME/KEY: Modified-site
         (B) LOCATION: 109
         (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,
               Met, Glu, Ser, or Leu"

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Cys Xaa Xaa Met Ile Asp Glu Xaa Ile Xaa Xaa Leu Lys Xaa Xaa
1   5   10   15

Pro Xaa Pro Xaa Xaa Asp Phe Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa
          20   25   30

Ile Leu Met Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Glu Ala Phe Xaa

                              50

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                35                      40                      45

Arg Xaa Xaa Lys Xaa Xaa Xaa Asn Ala Ser Ala Ile Glu Xaa Xaa Leu
    50                      55                      60

Xaa Xaa Leu Xaa Pro Cys Leu Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg
65                      70                      75                      80

Xaa Pro Ile Xaa Xaa Xaa Xaa Gly Asp Trp Xaa Glu Phe Xaa Xaa Lys
                85                      90                      95

Leu Xaa Phe Tyr Leu Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln
            100                     105                     110
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 133 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 1
        (D) OTHER INFORMATION: /note= "Met- may or may not precede
            the amino acid in position 1"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 18
        (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn
            or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 19
        (D) OTHER INFORMAITON: /note= "Xaa at position 19 is Met,
            Ala, or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 20
        (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile,
            Pro, or Leu"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 23
        (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,
            Ala, or Leu"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 25
        (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr
            or His"

51

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 29
    (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
        Arg, Val, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 32
    (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
        Ala, Asn, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 34
    (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 37
    (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
        Pro, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION; 38
    (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 42
    (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
        Ala, Ser, Asp, or Asn"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 45
    (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
        Val, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 46
    (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 49
    (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,
        Ile, Leu, or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 50
    (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu
        or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 51

```
            (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,
                    Arg, or Ser"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 55
            (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,
                    Leu, or Thr"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 56
            (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro
                    or Ser"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 59
            (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu
                    or Leu"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 60
            (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala
                    or Ser"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 62
            (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn
                    Val, or Pro"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 63
            (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg
                    or His"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 65
            (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val
                    or Ser"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 67
            (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,
                    Asn, His, or Gln"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 69
            (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln
                    or Glu"

    (ix) FEATURE:
            (A) NAME/KEY: Modified-site
            (B) LOCATION: 73
            (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala
```

or Gly"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 76
        (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
            Ala, or Pro"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 79
        (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,
            Arg, or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 82
        (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
            Glu, Val, or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 85
        (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu
            or Val"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 87
        (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu,
            Ser, or Tyr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 88
        (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
            or Trp"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 91
        (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
            or Pro"
(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 93
        (D) OTHER INFORMATION: /note= "Xaa at position 93 is Pro
            or Ser"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 95
        (D) OTHER INFORMATION: /note= "Xaa at position 95 is His
            or Thr"

(ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 98
        (D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
            Ile, or Thr"

```
(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 100
     (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys
         or Arg"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 101
     (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
         Ala, or Met"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 105
     (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn
         or Glu"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 109
     (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
         Glu, or Leu"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 112
     (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr
         or Gln"
(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 116
     (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
         Val, Trp, or Ser"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 117
     (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr
         or Ser"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 120
     (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
         Gln, or His"

(ix) FEATURE:
     (A) NAME/KEY: Modified-site
     (B) LOCATION: 123
     (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala
         or Glu"


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1               5                   10                  15

Ser Xaa Xaa Xaa Asp Glu Xaa Ile Xaa His Leu Lys Xaa Pro Pro Xaa
            20                  25                  30
```

55

```
Pro Xaa Leu Asp Xaa Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa Ile Leu
    35                  40              45

Xaa Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Xaa Xaa Phe Xaa Xaa Ala
    50                  55              60

Xaa Lys Xaa Leu Xaa Asn Ala Ser Xaa Ile Glu Xaa Ile Leu Xaa Asn
65                  70              75                  80

Leu Xaa Pro Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Pro
            85              90                  95

Ile Xaa Ile Xaa Xaa Gly Asp Trp Xaa Glu Phe Arg Xaa Lys Leu Xaa
        100             105             110

Phe Tyr Leu Xaa Xaa Leu Glu Xaa Ala Gln Xaa Gln Gln Thr Thr Leu
        115             120             125

Ser Leu Ala Ile Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 1
        (D) OTHER INFORMATION: /note= "Met- or Met-Ala may or may
             not precede the amino acid in position 1"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 4
        (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn or
             Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 5
        (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met,
             Ala, or Ile"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 6
        (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile,
             Pro, or Leu"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 9
        (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile,
             Ala, or Leu"

(ix) FEATURE:
    (A) NAM/KEY: Modified-site
    (B) LOCATION: 11
    (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr
        or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 15
    (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,
        Arg, Val, or Ile"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 18
    (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
        Ala, Asn, or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 20
    (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 23
    (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
        Pro, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 24
    (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
        or Ala"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 28
    (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
        Ala, Ser, Asp, or Asn"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 31
    (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
        Val, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 32
    (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 35
    (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met,
        Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu
    or Asp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 37
    (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
        Arg, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 41
    (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
        Leu, or Thr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION 42
    (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 45
    (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu
        or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 46
    (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 48
    (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
        Val, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 49
    (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg
        or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 51
    (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 53
    (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
        Asn, His, or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 55
    (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln

or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 59
    (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala
        or Gly"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 62
    (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
        Ala, or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 65
    (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
        Arg, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 67
    (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,
        Glu, or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 68
    (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
        Glu, Val, or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION 71
    (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu
        or Val"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 73
    (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu,
        Ser, or Tyr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 74
    (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala
        or Trp"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 77
    (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala
        or Pro"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 79
    (D) OTHER INFORMATION: /note= "Xaa at position 79 is Pro
        or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 81
    (D) OTHER INFORMATION: /note= "Xaa at position 81 is His
        or Thr"
(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 84
    (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,
        Ile, or Thr"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 86
    (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys
        or Arg"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 87
    (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,
        Ala, or Met"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 91
    (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn
        or Glu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 95
    (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
        Glu, or Leu"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 98
    (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr
        or Gln"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 102
    (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,
        Val, Trp, or Ser"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 103
    (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr
        or Ser"
(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 106
    (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
        Gln, or His"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site

(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Asn Cys Ser Xaa Xaa Xaa Asp Glu Xaa Ile Xaa His Leu Lys Xaa Pro
1               5               10              15

Pro Xaa Pro Xaa Leu Asp Xaa Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa
        20              25              30

Ile Leu Xaa Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Xaa Xaa Phe Xaa
        35              40              45

Xaa Ala Xaa Lys Xaa Leu Xaa Asn Ala Ser Xaa Ile Glu Xaa Ile Leu
    50              55              60

Xaa Asn Xaa Xaa Pro Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg
65              70              75              80

Xaa Pro Ile Xaa Ile Xaa Xaa Gly Asp Trp Xaa Glu Phe Arg Xaa Lys
        85              90              95

Leu Xaa Phe Tyr Leu Xaa Xaa Leu Glu Xaa Ala Gln Xaa Gln Gln
        100             105             110
```

(2) INFORMATION FOR SEQ ID NO:9:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 111 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
1               5               10              15

Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp
        20              25              30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
        35              40              45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
    50              55              60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65              70              75              80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
        85              90              95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
        100             105             110
```

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(2) INFORMATION FOR SEQ ID NO:10:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 111 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

      Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
      1   5   10   15

      Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp
                      20   25   30

      Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
                  35   40   45

      Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
          50   55   60

      Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
      65   70   75   80

      His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                      85   90   95

      Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                      100   105   110

(2) INFORMATION FOR SEQ ID NO:11:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 111 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

      Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Val Pro
      1   5   10   15

      Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp Met Asp
                      20   25   30

      Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
                  35   40   45

      Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
          50   55   60

      Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg

```
              65                    70                   75                   80

        His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                            85                   90                   95

        Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                          100                  105                  110
```

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
        Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
        1               5                   10                   15

        Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
                          20                  25                   30

        Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val
                          35                  40                   45

        Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
                 50                  55                  60

        Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
        65                   70                  75                   80

        His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                            85                   90                   95

        Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                          100                  105                  110
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
        Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
        1               5                   10                   15

        Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
                          20                  25                   30
```

```
            Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val
                    35              40              45

            Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
                50              55              60

            Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
            65              70              75              80

            His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                            85              90              95

            Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                        100             105             110
```

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
            Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
            1               5               10              15

            Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
                        20              25              30

            Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val
                    35              40              45

            Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
                50              55              60

            Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
            65              70              75              80

            His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                            85              90              95

            Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                        100             105             110
```

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

64

```
Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1               5                   10                  15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
            20                  25                  30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
            35                  40                  45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
        50                  55                  60

Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65                  70                  75                      80

His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Arg Lys
                85                  90                  95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:16:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1               5                   10                  15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
            20                  25                  30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
            35                  40                  45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
        50                  55                  60

Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65                  70                  75                      80

His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Arg Lys
                85                  90                  95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:17:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid

65

(D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

     Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
     1   5   10   15

     Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
                     20   25   30

     Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
                 35   40   45

     Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
             50   55   60

     Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
     65   70   75   80

     His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys
                     85   90   95

     Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
                     100   105   110

(2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 111 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

     Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
     1   5   10   15

     Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
                     20   25   30

     Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
                 35   40   45

     Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
             50   55   60

     Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
     65   70   75   80

     His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys
                     85   90   95

     Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1               5                   10                  15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
            20                  25                  30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
        35                  40                  45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
    50                  55                  60

Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65              70                  75                  80

His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys
            85                  90                  95

Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1               5                   10                  15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
            20                  25                  30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
        35                  40                  45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
    50                  55                  60
```

```
Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65              70              75              80

His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys
                85              90              95

Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
                100             105             110
```

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1               5               10              15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
                20              25              30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
            35              40              45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
    50              55              60

Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65              70              75              80

His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys
                85              90              95

Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln
                100             105             110
```

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
1               5               10              15

Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp
                20              25              30
```

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```
Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val
        35                  40                  45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
    50                  55                  60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65                  70                  75                  80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                85                  90                  95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:23:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
1               5               10                  15

Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp
            20                  25                  30

Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val
        35                  40                  45

Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
    50                  55                  60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65                  70                  75                  80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
                85                  90                  95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
                100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:24:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

69
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Val Pro
1                   5                   10                  15

Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp Met Asp
            20                  25                  30

Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val
        35                  40                  45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
    50                  55                  60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65                  70                  75                  80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
            85                  90                  95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
            100                 105                 110

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1                   5                   10                  15

Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
            20                  25                  30

Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
        35                  40                  45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala
    50                  55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85                  90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100                 105                 110

Gln


(2) INFORMATION FOR SEQ ID NO:26:

(i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH: 113 amino acids
             (B)  TYPE: amino acid
             (D)  TOPOLOGY: linear

       (ii)  MOLECULE TYPE: peptide


       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:26:

    Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
    1               5                   10                  15

    Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
                20                  25                  30

    Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
                35                  40                  45

    Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala
        50                  55                  60

    Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
    65                  70                  75                  80

    Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                    85                  90                  95

    Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                100                 105                 110

    Gln


  (2)  INFORMATION FOR SEQ ID NO:27:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH: 113 amino acids
             (B)  TYPE: amino acid
             (D)  TOPOLOGY: linear

       (ii)  MOLECULE TYPE: peptide


       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:27:

    Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
    1               5                   10                  15

    Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
                20                  25                  30

    Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
                35                  40                  45

    Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala
        50                  55                  60

```
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75                      80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
            100             105             110

Gln
```

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10                      15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
            20              25              30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser
    50              55              60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65              70              75                      80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
                85              90                  95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
            100             105             110

Gln
```

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                      15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20                  25                  30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35                  40                  45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser
    50                  55                  60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65                  70                  75                      80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
            85                  90                  95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
            100                 105                 110

Gln
```

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                      15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
            20                  25                  30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
        35                  40                  45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser
    50                  55                  60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65                  70                  75                      80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
            85                  90                  95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
            100                 105                 110

Gln
```

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(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                  15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
            20              25              30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105                 110

Gln
```

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
```

```
                50                    55                   60

        Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
        65                  70                  75                  80

        Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                        85                  90                  95

        Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                        100                 105                 110

        Gln


(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

        Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
        1                   5                   10                  15

        Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
                        20                  25                  30

        Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
                        35                  40                  45

        Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
                        50                  55                  60

        Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
        65                  70                  75                  80

        Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                        85                  90                  95

        Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                        100                 105                 110

        Gln


(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
            20              25              30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35          .       40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln
```

(2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110
```

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Gln

(2) INFORMATION FOR SEQ ID NO:36:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 113 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

      Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
      1   5   10   15

      Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                      20   25   30

      Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
                  35   40   45

      Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50   55   60

      Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
      65   70   75   80

      Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                      85   90   95

      Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
                  100   105   110

      Gln

(2) INFORMATION FOR SEQ ID NO:37:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 113 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

      Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
      1   5   10   15

      Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
                      20   25   30

      Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
                  35   40   45

77

```
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50                  55              60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70              75                      80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                      95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
            100             105             110

Gln
```

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50                  55              60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70              75                      80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                      95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln
```


(2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
            20   25   30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
            35   40   45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
            100   105   110

Gln

(2) INFORMATION FOR SEQ ID NO:40:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 113 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
            20   25   30

Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser
            35   40   45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln

79

Gln

(2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20   25   30

Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35   40   45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20   25   30

```
Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
        100             105             110

Gln
```

(2) INFORMATION FOR SEQ ID NO:43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
            20              25              30

Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
            35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
        100             105             110

Gln
```

(2) INFORMATION FOR SEQ ID NO:44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20   25   30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35   40   45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln

(2) INFORMATION FOR SEQ ID NO:45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

    Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
    1   5   10   15

    Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
                20   25   30

    Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
            35   40   45

    Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

    Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
    65   70   75   80

    Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

82

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln

(2) INFORMATION FOR SEQ ID NO:46:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 125 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

     Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Lys Asn Cys
     1   5   10   15

     Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Ala
                 20   25   30

     Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp Ile Leu
                 35   40   45

     Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
         50   55   60

     Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
     65   70   75   80

     Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
                 85   90   95

     Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
                 100   105   110

     Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
             115   120   125

(2) INFORMATION FOR SEQ ID NO:47:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 125 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

     Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys Asn Cys
     1   5   10   15

     Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn

83

```
Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu
        35              40                  45

Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala
    50              55                  60

Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
65              70                  75                      80

Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
            85              90                  95

Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
            100             105                 110

Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
        115             120                 125
```

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys
1               5               10                  15

Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
            20              25                  30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
            35              40                  45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70                  75                      80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105                 110

Gln
```

(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 134 amino acids

(B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

    Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
    1   5   10   15

    Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro
                    20   25   30

    Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile
                35   40   45

    Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg
            50   55   60

    Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys
    65   70   75   80

    Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His
                    85   90   95

    Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu
                    100   105   110

    Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr
            115   120   125

    Leu Ser Leu Ala Ile Phe
        130

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

    Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
    1   5   10   15

    Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
                    20   25   30

    Gly Gly Gly Ser
            35

85

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
1   5   10   15

Ser Lys Glu Ser His Lys Ser Pro
            20

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Glu Gly Arg Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
1   5   10   15

Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
            20   25

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 906 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTAGG CCCTGCCAGC   420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTGC TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT   480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG   540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG   600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG   660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG   720

CTGGACGTCG CCGACTTTGC CACCACCATC TAACTGGGAA TGGCCCCTGC CCTGCAGCCC   780

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG   840

GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG   900

                                                                          906
CAGCCC

(2) INFORMATION FOR SEQ ID NO:54:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 732 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT   420

GAAATTATAC ATCACTTAAA GAGACCACCT AACCCTTTGC TGGACCCGAA CAACCTCAAT   480

TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC   540

GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC   600

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA   660

GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG   720

CAGGAACAAC AG   732

(2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 777 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCAC CGGCTCGTTC CCCGTCCCCG   420

TCTACCCAGC CGTGGGAACA CGTGAATGCC ATCCAGGAGG CCCGGCGTCT CCTGAACCTG   480

AGTAGAGACA CTGCTGCTGA GATGAATGAA ACAGTAGAAG TGATATCAGA AATGTTTGAC   540

CTCCAGGAGC CGACTTGCCT ACAGACCCGC CTGGAGCTGT ACAAGCAGGG CCTGCGGGGC   600

AGCCTCACCA AGCTCAAGGG CCCCTTGACC ATGATGGCCA GCCACTACAA GCAGCACTGC   660

CCTCCAACCC CGGAAACTTC CTGTGCAACC CAGATTATCA CCTTTGAAAG TTTCAAAGAG   720

AACCTGAAGG ACTTCCTGCT TGTCATCCCC TTTGACTGCT GGGAGCCAGT CCAGGAG   777

(2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 921 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC     120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT     360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC     420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT     480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG     540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG     600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG     660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG     720

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC     780

CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG     840

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT     900

CTACGCCACC TTGCGCAGCC C                                              921
```

(2) INFORMATION FOR SEQ ID NO:57:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 951 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC     120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT     360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CAGTACCACC AGGTGAAGAT     420
```

TCCAAAGATG TGGCCGCCCC ACACAGACAG CCACTCACCT CTTCAGAACG AATTGACAAA   480

CAAATTCGGT ACATCCTCGA CGGGATATCA GCCCTGAGAA AGGAGACATG TAACAAGAGT   540

AACATGTGTG AAAGCAGCAA AGAGGCGCTA GCAGAAAACA ACCTGAACCT TCCAAAGATG   600

GCTGAAAAAG ATGGATGCTT CCAATCCGGA TTCAATGAGG AGACTTGCCT GGTGAAAATC   660

ATCACTGGTC TTTTGGAGTT TGAGGTATAC CTCGAGTACC TCCAGAACAG ATTTGAGAGT   720

AGTGAGGAAC AAGCCAGAGC TGTGCAGATG TCGACAAAAG TCCTGATCCA GTTCCTGCAG   780

AAAAAGGCAA AGAATCTAGA TGCAATAACC ACCCCTGACC CAACCACAAA TGCATCCCTG   840

CTGACGAAGC TGCAGGCACA GAACCAGTGG CTGCAGGACA TGACAACTCA TCTCATTCTG   900

CGCAGCTTTA AGGAGTTCCT GCAGTCCAGC CTGAGGGCTC TTCGGCAAAT G   951

(2) INFORMATION FOR SEQ ID NO:58:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 732 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT   420

GAAATTATAC ATCACTTAAA GAGACCACCT AACCCTTTGC TGGACCCGAA CAACCTCAAT   480

TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC   540

GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC   600

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA   660

GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG   720

CAGGAACAAC AG   732

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 921 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC   420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT   480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG   540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG   600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG   660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG   720

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC   780

CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG   840

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT   900

CTACGCCACC TTGCGCAGCC C   921

    (2) INFORMATION FOR SEQ ID NO:60:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 921 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

91

```
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC      120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA      180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG      300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC      360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC      420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT      480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG      540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG      600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG      660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG      720

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC      780

CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG      840

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT      900

CTACGCCACC TTGCGCAGCC C                                              921
```

(2) INFORMATION FOR SEQ ID NO:61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 732 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC       60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC      120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA      180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG      300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC      360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT      420

GAAATTATAC ATCACTTAAA GAGACCACCT AACCCTTTGC TGGACCCGAA CAACCTCAAT      480
```

92

TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC   540

GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC   600

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA   660

GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG   720

CAGGAACAAC AG   732

    (2) INFORMATION FOR SEQ ID NO:62:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 777 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC   480

TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAACC TCAATTCTGA AGACATGGAT   540

ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTCGTAAG GGCTGTCAAG   600

CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC   660

TCTGCCACGG CCGCACCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA   720

TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG   777

    (2) INFORMATION FOR SEQ ID NO:63:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 777 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC     120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT     360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA     420

TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC     480

TTAAAGAGAC CACCTACCCC TTTGCTGGAC CCGAACAACC TCAATTCTGA AGACATGGAT     540

ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTCGTAAG GGCTGTCAAG     600

CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC     660

TCTGCCACGG CCGCACCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA     720

TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG       777
```

(2) INFORMATION FOR SEQ ID NO:64:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 777 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60
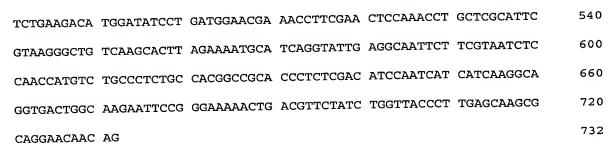
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC     120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC     360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA     420
```

```
TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC        480

TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAACC TCAATTCTGA AGACATGGAT        540

ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTCGTAAG GGCTGTCAAG        600

CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC        660

TCTGCCACGG CCGCACCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA        720

TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG          777
```

(2) INFORMATION FOR SEQ ID NO:65:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1047 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC         60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC        120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA        180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC        240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG        300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT        360

TCCCCCGGGC CTCCTGTCAA TGCTGGCGGC GGCTCTGGTG GTGGTTCTGG TGGCGGCTCT        420

GAGGGTGGCG GCTCTGAGGG TGGCGGTTCT GAGGGTGGCG GCTCTGAGGG TGGCGGTTCC        480

GGTGGCGGCT CCGGTTCCGG TGATTTTGAT TATGAAAACA TGGCTACACC ATTGGGCCCT        540

GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG        600

GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG        660

GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC        720

AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC        780

CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA        840

CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA        900

ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG        960

CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC       1020
```
```
                              95
```

CGCGTTCTAC GCCACCTTGC GCAGCCC

(2) INFORMATION FOR SEQ ID NO:66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 903 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC        60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC       120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA       180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC       240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG       300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT       360

TCCCCCGGGC CTCCTGTCAA TGCTGGCGGC GGCTCTGGTG GTGGTTCTGG TGGCGGCTCT       420

GAGGGTGGCG GCTCTGAGGG TGGCGGTTCT GAGGGTGGCG GCTCTGAGGG TGGCGGTTCC       480

GGTGGCGGCT CCGGTTCCGG TGATTTTGAT TATGAAAACA TGGCACCGGC TCGTTCCCCG       540

TCCCCGTCTA CCCAGCCGTG GGAACACGTG AATGCCATCC AGGAGGCCCG GCGTCTCCTG       600

AACCTGAGTA GAGACACTGC TGCTGAGATG AATGAAACAG TAGAAGTGAT ATCAGAAATG       660

TTTGACCTCC AGGAGCCGAC TTGCCTACAG ACCCGCCTGG AGCTGTACAA GCAGGGCCTG       720

CGGGGCAGCC TCACCAAGCT CAAGGGCCCC TTGACCATGA TGGCCAGCCA CTACAAGCAG       780

CACTGCCCTC CAACCCCGGA AACTTCCTGT GCAACCCAGA TTATCACCTT TGAAAGTTTC       840

AAAGAGAACC TGAAGGACTT CCTGCTTGTC ATCCCCTTTG ACTGCTGGGA GCCAGTCCAG       900

GAG                                                                   903
```

(2) INFORMATION FOR SEQ ID NO:67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1017 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
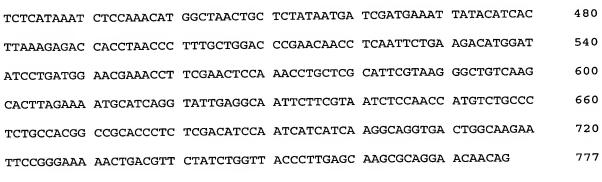ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC     120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT     360

TCCCCCGGTG GCGGCGGCTC TGGTGGTGGT TCTGGTGGCG GCTCTGAGGG TGGCGGCTCT     420

GAGGGTGGCG GTTCTGAGGG TGGCGGCTCT GAGGGTGGCG GTTCCGGTGG CGGCTCCGGT     480

TCCGGTAACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC     540

AAGTGCTTAG AGCAAGTGAG GAAGATCCAG GGCGATGGCG CAGCGCTCCA GGAGAAGCTG     600

TGTGCCACCT ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC     660

ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG     720

AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC TGCAGGCCCT GGAAGGGATA     780

TCCCCCGAGT TGGGTCCCAC CTTGGACACA CTGCAGCTGG ACGTCGCCGA CTTTGCCACC     840

ACCATCTGGC AGCAGATGGA AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT     900

GCCATGCCGG CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC     960

CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC GCAGCCC      1017
```

(2) INFORMATION FOR SEQ ID NO:68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 966 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC     120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300
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TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC   480

TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG   540

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC   600

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA   660

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG   720

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC   780

TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC   840

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG   900

GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG   960

CAGCCC   966

(2) INFORMATION FOR SEQ ID NO:69:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 822 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCACCGGCT CGTTCCCCGT CCCCGTCTAC CCAGCCGTGG   480

GAACACGTGA ATGCCATCCA GGAGGCCCGG CGTCTCCTGA ACCTGAGTAG AGACACTGCT   540

GCTGAGATGA ATGAAACAGT AGAAGTGATA TCAGAAATGT TTGACCTCCA GGAGCCGACT   600

TGCCTACAGA CCCGCCTGGA GCTGTACAAG CAGGGCCTGC GGGGCAGCCT CACCAAGCTC   660

AAGGGCCCCT TGACCATGAT GGCCAGCCAC TACAAGCAGC ACTGCCCTCC AACCCCGGAA   720

ACTTCCTGTG CAACCCAGAT TATCACCTTT GAAAGTTTCA AAGAGAACCT GAAGGACTTC   780

CTGCTTGTCA TCCCCTTTGA CTGCTGGGAG CCAGTCCAGG AG   822

(2) INFORMATION FOR SEQ ID NO:70:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 966 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC   480

TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG   540

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC   600

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA   660

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG   720

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC   780

TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC   840

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG   900

GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG   960

CAGCCC   966

(2) INFORMATION FOR SEQ ID NO:71:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 966 base pairs
            (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC   480

TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG   540

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC   600

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA   660

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG   720

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC   780

TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC   840

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG   900

GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG   960

CAGCCC
                                                                     966

(2) INFORMATION FOR SEQ ID NO:72:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 921 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA   60

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GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC          120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG          180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC          240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG          300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG          360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG          420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG          480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG          540

GGAAGGATTT CCCCGGGTGG TGGTTCTGGC GGCGGCTCCA ACATGGCTAA CTGCTCTATA          600

ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC          660

AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG          720

CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT          780

CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC          840

ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT          900

GAGCAAGCGC AGGAACAACA G                                                   921

(2)  INFORMATION FOR SEQ ID NO:73:

         (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 966 base pairs
              (B)  TYPE: nucleic acid
              (C)  STRANDEDNESS: double
              (D)  TOPOLOGY: linear

         (ii)  MOLECULE TYPE: DNA (genomic)



         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA           60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC          120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG          180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC          240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG          300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG          360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG          420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG          480
```

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG   540

GGAAGGATTT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG   600

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT   660

ATACATCACT TAAAGAGACC ACCTAACCCT TTGCTGGACC CGAACAACCT CAATTCTGAA   720

GACATGGATA TCCTGATGGA ACGAAACCTT CGAACTCCAA ACCTGCTCGC ATTCGTAAGG   780

GCTGTCAAGC ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA   840

TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC   900

TGGCAAGAAT TCCGGGAAAA ACTGACGTTC TATCTGGTTA CCCTTGAGCA AGCGCAGGAA   960

CAACAG   966

(2) INFORMATION FOR SEQ ID NO:74:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1047 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA   60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC   120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG   180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC   240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG   300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG   360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG   420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG   540

GGAAGGATTT CCCCCGGGCC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT   600

GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT   660

GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTTGATT ATGAAAACAT GGCTAACTGC   720

TCTATAATGA TCGATGAAAT TATACATCAC TTAAAGAGAC CACCTAACCC TTTGCTGGAC   780

CCGAACAACC TCAATTCTGA AGACATGGAT ATCCTGATGG AACGAAACCT TCGAACTCCA   840

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AACCTGCTCG CATTCGTAAG GGCTGTCAAG CACTTAGAAA ATGCATCAGG TATTGAGGCA   900

ATTCTTCGTA ATCTCCAACC ATGTCTGCCC TCTGCCACGG CCGCACCCTC TCGACATCCA   960

ATCATCATCA AGGCAGGTGA CTGGCAAGAA TTCCGGGAAA AACTGACGTT CTATCTGGTT   1020

ACCCTTGAGC AAGCGCAGGA ACAACAG   1047

    (2) INFORMATION FOR SEQ ID NO:75:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 921 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA   60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC   120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG   180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC   240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG   300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG   360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG   420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG   540

GGAAGGATTT CCCCGGGTGG TGGTTCTGGC GGCGGCTCCA ACATGGCTAA CTGCTCTATA   600

ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG CACCTTTGCT GGACCCGAAC   660

AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGAACGAA ACCTTCGACT TCCAAACCTG   720

GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT   780

CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC   840

ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT   900

GAGCAAGCGC AGGAACAACA G   921

    (2) INFORMATION FOR SEQ ID NO:76:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1047 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA   60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC   120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG   180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC   240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG   300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG   360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG   420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG   540

GGAAGGATTT CCCCCGGGCC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT   600

GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT   660

GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTTGATT ATGAAAACAT GGCTAACTGC   720

TCTATAATGA TCGATGAAAT TATACATCAC TTAAAGAGAC CACCTGCACC TTTGCTGGAC   780

CCGAACAACC TCAATGACGA AGACGTCTCT ATCCTGATGG AACGAAACCT TCGACTTCCA   840

AACCTGGAGA GCTTCGTAAG GGCTGTCAAG AACTTAGAAA ATGCATCAGG TATTGAGGCA   900

ATTCTTCGTA ATCTCCAACC ATGTCTGCCC TCTGCCACGG CCGCACCCTC TCGACATCCA   960

ATCATCATCA AGGCAGGTGA CTGGCAAGAA TTCCGGGAAA AACTGACGTT CTATCTGGTT   1020

ACCCTTGAGC AAGCGCAGGA ACAACAG   1047

    (2) INFORMATION FOR SEQ ID NO:77:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 966 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA   60

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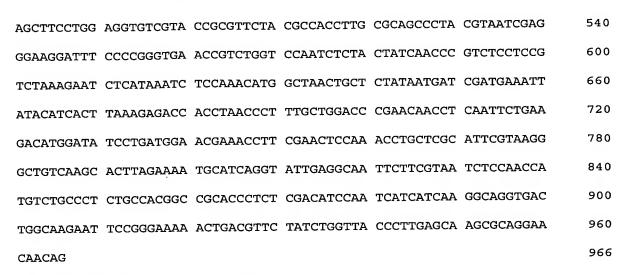GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC    120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG    180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC    240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG    300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG    360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG    420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG    480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG    540

GGAAGGATTT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG    600

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT    660

ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA    720

GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG    780

GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA    840

TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC    900

TGGCAAGAAT TCCGGGAAAA ACTGACGTTC TATCTGGTTA CCCTTGAGCA AGCGCAGGAA    960

CAACAG                                                               966
```

(2) INFORMATION FOR SEQ ID NO:78:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 921 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA     60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC    120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG    180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC    240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG    300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG    360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG    420
```

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC   540

GGTGGAGGCT CCCCGGGTGG TGGTTCTGGC GGCGGCTCCA ACATGGCTAA CTGCTCTATA   600

ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG CACCTTTGCT GGACCCGAAC   660

AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGAACGAA ACCTTCGACT TCCAAACCTG   720

GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT   780

CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC   840

ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT   900

GAGCAAGCGC AGGAACAACA G   921

(2) INFORMATION FOR SEQ ID NO:79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 966 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA   60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC   120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG   180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC   240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG   300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG   360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CACCCAGGG TGCCATGCCG   420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC   540

GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG   600

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT   660

ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA   720

GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG   780

GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA   840

106

TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC   900

TGGCAAGAAT TCCGGGAAAA ACTGACGTTC TATCTGGTTA CCCTTGAGCA AGCGCAGGAA   960

CAACAG   966

(2) INFORMATION FOR SEQ ID NO:80:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 921 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA   60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC   120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG   180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC   240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG   300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG   360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG   420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC   540

GGTGGAGGCT CCCCGGGTGG TGGTTCTGGC GGCGGCTCCA ACATGGCTAA CTGCTCTATA   600

ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG CACCTTTGCT GGACCCGAAC   660

AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGAACGAA ACCTTCGACT TCCAAACCTG   720

GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT   780

CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC   840

ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT   900

GAGCAAGCGC AGGAACAACA G   921

(2) INFORMATION FOR SEQ ID NO:81:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 966 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA        60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC       120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG       180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC       240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG       300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG       360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG       420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG       480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC       540

GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG       600

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT       660

ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA       720

GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG       780

GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA       840

TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC       900

TGGCAAGAAT TCCGGGAAAA ACTGACGTTC TATCTGGTTA CCCTTGAGCA AGCGCAGGAA       960

CAACAG                                                                  966
```

(2) INFORMATION FOR SEQ ID NO:82:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 777 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA        60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC       120
```

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC   480

TTAAAGAGAC CACCTGCACC TTTGCTGGAC CCGAACAACC TCAATGACGA AGACGTCTCT   540

ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTGGAGA GCTTCGTAAG GGCTGTCAAG   600

AACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC   660

TCTGCCACGG CCGCACCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA   720

TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG   777

(2) INFORMATION FOR SEQ ID NO:83:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 984 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA   60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC   120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTACACCA TTGGGCCCTG CCAGCTCCCT GCCCCAGAGC   480

TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG   540

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC   600

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA   660

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG   720

```
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC        780

TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC        840

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG        900

GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG        960

CAGCCCTGAT AAGGATCCGA ATTC                                             984
```

(2) INFORMATION FOR SEQ ID NO:84:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 921 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA         60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC        120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA        180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC        240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG        300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT        360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTAGG CCCTGCCAGC        420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTGC TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT        480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG        540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG        600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG        660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG        720

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC        780

CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG        840

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT        900

CTACGCCACC TTGCGCAGCC C                                                921
```

(2) INFORMATION FOR SEQ ID NO:85:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 921 base pairs

```
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: double
          (D)  TOPOLOGY: linear

     (ii)  MOLECULE TYPE: DNA (genomic)




     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA      60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC     120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA     180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC     240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG     300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT     360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC     420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT     480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG     540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG     600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG     660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG     720

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC     780

CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG     840

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT     900

CTACGCCACC TTGCGCAGCC C                                              921

(2)  INFORMATION FOR SEQ ID NO:86:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 732 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: double
          (D)  TOPOLOGY: linear
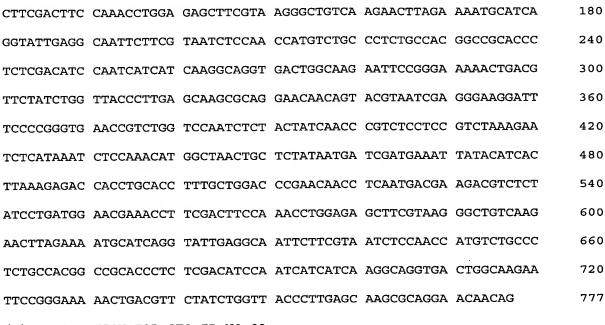
     (ii)  MOLECULE TYPE: DNA (genomic)




     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA      60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC     120
```

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT   420

GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT   480

GACGAAGACG TCTCTATCCT GATGGAACGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC   540

GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC   600

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA   660

GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG   720

CAGGAACAAC AG   732

(2) INFORMATION FOR SEQ ID NO:87:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 921 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA   60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC   120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC   420

TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT   480

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG   540

GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG   600

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG   660

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG   720

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```
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC      780

CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG      840

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT      900

CTACGCCACC TTGCGCAGCC C                                                921
```

(2) INFORMATION FOR SEQ ID NO:88:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 732 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA       60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC      120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA      180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG      300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC      360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT      420

GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT      480

GACGAAGACG TCTCTATCCT GATGGAACGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC      540

GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC      600

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA      660

GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG      720

CAGGAACAAC AG                                                         732
```

(2) INFORMATION FOR SEQ ID NO:89:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 966 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA        60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC       120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA       180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC       240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG       300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC       360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA       420

TCTCATAAAT CTCCAAACAT GGCTACACCA TTGGGCCCTG CCAGCTCCCT GCCCCAGAGC       480

TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG       540

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC       600

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA       660

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG       720

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC       780

TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC       840

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG       900

GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG       960

CAGCCC                                                                  966
```

(2) INFORMATION FOR SEQ ID NO:90:

> (i) SEQUENCE CHARACTERISTICS:
>   (A) LENGTH: 777 base pairs
>   (B) TYPE: nucleic acid
>   (C) STRANDEDNESS: double
>   (D) TOPOLOGY: linear
>
> (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA        60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC       120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA       180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC       240
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TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420

TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC   480

TTAAAGAGAC CACCTGCACC TTTGCTGGAC CCGAACAACC TCAATGACGA AGACGTCTCT   540

ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTGGAGA GCTTCGTAAG GGCTGTCAAG   600

AACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC   660

TCTGCCACGG CCGCACCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA   720

TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG   777

(2) INFORMATION FOR SEQ ID NO:91:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 41 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: other nucleic acid
             (A) DESCRIPTION: /desc = "synthetic DNA"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AATTCCGGGA AAAACTGACG TTCTATCTGG TTACCCTTGA G   41

(2) INFORMATION FOR SEQ ID NO:92:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 46 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: other nucleic acid
             (A) DESCRIPTION: /desc = "synthetic DNA"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGCGCTTGC TCAAGGGTAA CCAGATAGAA CGTCAGTTTT TCCCGG   46

(2) INFORMATION FOR SEQ ID NO:93:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 39 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
              (A) DESCRIPTION: /desc = "synthetic DNA"

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAAGCGCAGG AACAACAGTA CGTAATCGAG GGAAGGATT   39

(2) INFORMATION FOR SEQ ID NO:94:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 39 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: other nucleic acid
              (A) DESCRIPTION: /desc = "synthetic DNA"

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ACCCGGGGAA ATCCTTCCCT CGATTACGTA CTGTTGTTC   39

(2) INFORMATION FOR SEQ ID NO:95:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 63 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: other nucleic acid
              (A) DESCRIPTION: /desc = "synthetic DNA"

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGTAAG GTACCGCATG CAAGCTTAGA   60

TCT   63

(2) INFORMATION FOR SEQ ID NO:96:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 58 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: other nucleic acid
              (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AGCTAGATCT AAGCTTGCAT GCGGTACCTT ACATGTTGGA GCCGCCGCCA GAACCACC   58

(2) INFORMATION FOR SEQ ID NO:97:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 74 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   60

CATAAATCTC CAAA   74

(2) INFORMATION FOR SEQ ID NO:98:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 74 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGTTTGGA GATTTATGAG ATTCTTTAGA CGGAGGAGAC GGGTTGATAG TAGAGATTGG   60

ACCAGACGGT TCAC   74

(2) INFORMATION FOR SEQ ID NO:99:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 68 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC   60

CCTACGTA   68

(2) INFORMATION FOR SEQ ID NO:100:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 68 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: other nucleic acid
             (A) DESCRIPTION: /desc = "synthetic DNA"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AGCTTACGTA GGGCTGCGCA AGGTGGCGTA GAACGCGGTA CGACACCTCC AGGAAGCTCT   60

GCAGATGG   68

(2) INFORMATION FOR SEQ ID NO:101:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 21 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: other nucleic acid
             (A) DESCRIPTION: /desc = "synthetic DNA"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTAATCGAGG GAAAGATTTC C   21

(2) INFORMATION FOR SEQ ID NO:102:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 25 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: other nucleic acid
             (A) DESCRIPTION: /desc = "synthetic DNA"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCGGGGAAAT CTTTCCCTCG ATTAC   25

(2) INFORMATION FOR SEQ ID NO:103:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTAGAGGGCG GTGGAGGCTC C   21

(2) INFORMATION FOR SEQ ID NO:104:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CCGGGGAGCC TCCACCGCCC TCTAC   25

(2) INFORMATION FOR SEQ ID NO:105:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "sythetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CATGGCACCA GCAAGATCAC CATCACCATC AACTCAACCT TGGGAACATG TGAATGCC   58

(2) INFORMATION FOR SEQ ID NO:106:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATTCACATG TTCCCAAGGT TGAGTTGATG GTGATGGTGA TCTTGCTGGT GC   52

(2) INFORMATION FOR SEQ ID NO:107:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 66 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC   60

AGGGCG   66

(2) INFORMATION FOR SEQ ID NO:108:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 66 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGGATCTTC CTCACTTGCT CTAAAGACTT GAGCAGGAAG CTCTGGGGCA GGGAGCTGGC   60

AGGGCC   66

(2) INFORMATION FOR SEQ ID NO:109:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 48 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AGCTTACCTG CCATGGCTCC AGTACCACCA GGTGAAGATT CCAAAGAT   48

(2) INFORMATION FOR SEQ ID NO:110:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TTGGAATCTT CACCTGGTGG TACTGGAGCC ATGGCAGGTA   40

(2) INFORMATION FOR SEQ ID NO:111:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCTTCCATG GCTACCCCCC TGGGCC   26

(2) INFORMATION FOR SEQ ID NO:112:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAGGGGGGTA GCCATGGA   18

(2) INFORMATION FOR SEQ ID NO:113:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CATGGCTACA CCATTGGGCC   20

(2) INFORMATION FOR SEQ ID NO:114:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAATGGTGTA GC   12

(2) INFORMATION FOR SEQ ID NO:115:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCTACA CCATTAGGAC   20

(2) INFORMATION FOR SEQ ID NO:116:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear '

    (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TAATGGTGTA GC   12

(2) INFORMATION FOR SEQ ID NO:117:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CCTGTCAACC CGGGCGGCGG CTCTGGTGGT   30

(2) INFORMATION FOR SEQ ID NO:118:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TCATAATACA TGTTACCGGA ACGGAGCCGC C   31

(2) INFORMATION FOR SEQ ID NO:119:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 34 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATCGTCTGAC CTCCCGGGAC CTCCTGTCAA TGCT   34

(2) INFORMATION FOR SEQ ID NO:120:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AGCGTTTGAC ATGTTTTCAT AATCAAAATC   30

(2) INFORMATION FOR SEQ ID NO:121:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
        20   25   30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35   40   45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115   120   125

124

```
Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
    130                 135             140
```

```
Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145             150             155                     160
```

```
Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
            165             170             175
```

```
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
            180             185             190
```

```
Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
            195             200             205
```

```
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
    210             215             220
```

```
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225             230             235             240
```

```
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
            245             250             255
```

```
Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
            260             265             270
```

```
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
            275             280             285
```

```
His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
    290             295             300
```

```
Ala Gln Pro
305
```

(2) INFORMATION FOR SEQ ID NO:122:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10                      15
```

```
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30
```

```
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
            35              40              45
```

```
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75                          80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                      95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115             120             125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
    130             135             140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145             150             155             160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
                165             170             175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
        180             185             190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
        195             200             205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
    210             215             220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225             230             235             240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
                245             250             255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
            260             265             270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
        275             280             285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
    290             295             300

Ala Gln Pro
305
```

(2) INFORMATION FOR SEQ ID NO:123:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
              20   25   30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35   40   45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
              85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100   105   110

Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115   120   125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
    130   135   140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145   150   155   160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
              165   170   175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
              180   185   190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
          195   200   205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
    210   215   220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225   230   235   240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
              245   250   255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
          260   265   270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
        275   280   285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
    290   295   300

127

Ala Gln Pro
305

(2) INFORMATION FOR SEQ ID NO:124:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20   25   30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35   40   45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
        115   120   125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
    130   135   140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145   150   155   160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
            165   170   175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
            180   185   190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
            195   200   205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
    210   215   220

128

```
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225             230             235             240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
                245             250             255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
                260             265             270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
            275             280             285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
    290             295             300

Ala Gln Pro
305
```

(2) INFORMATION FOR SEQ ID NO:125:

  (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 244 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: protein

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1             5             10             15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20             25             30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35             40             45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50             55             60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65             70             75             80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85             90             95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115             120             125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
    130             135             140

His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn
```

Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn
                165   170   175

Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
            180   185   190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
            195   200   205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
        210   215   220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225   230   235   240

Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:126:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

    Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
    1   5   10   15

    Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                  20   25   30

    Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35   40   45

    Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

    Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
    65   70   75   80

    Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                      85   90   95

    Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                  100   105   110

    Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Gly Ser Gly Gly
                  115   120   125

    Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
        130   135   140

```
His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn
145             150             155                     160

Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn
                165             170                 175

Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
            180             185                 190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
            195             200             205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
    210             215             220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225             230             235             240

Gln Glu Gln Gln
```

(2) INFORMATION FOR SEQ ID NO:127:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
        115             120             125
```

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```
Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
    130             135         140

His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn
145             150             155                 160

Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn
            165             170             175

Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
            180             185             190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
        195             200             205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
    210             215             220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225             230             235                 240

Gln Glu Gln Gln
```

(2) INFORMATION FOR SEQ ID NO:128:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 322 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
```

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```
                 115                    120                     125
     Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
         130                 135                 140

     Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
     145                 150                 155                     160

     Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
                 165                 170                 175

     Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
                 180                 185                 190

     Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
                 195                 200                 205

     Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
         210                 215                 220

     Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
     225                 230                 235                     240

     Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
                 245                 250                 255

     Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
                 260                 265                 270

     Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
         275                 280                 285

     Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
         290                 295                 300

     Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
     305                 310                 315                     320

     Gln Pro
```

(2) INFORMATION FOR SEQ ID NO:129:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 322 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
     Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
     1                 5                   10                  15

     Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                 20                  25                  30
```

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```
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75                      80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                      95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro
        115             120             125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130             135             140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
145             150             155             160

Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
            165             170             175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
            180             185             190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
        195             200             205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
    210             215             220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
225             230             235             240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
            245             250             255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
            260             265             270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
        275             280             285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
        290             295             300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
305             310             315             320

Gln Pro
```

(2) INFORMATION FOR SEQ ID NO:130:

    (i) SEQUENCE CHARACTERISTICS:

134

```
    (A)  LENGTH: 322 amino acids
    (B)  TYPE: amino acid
    (C)  STRANDEDNESS:
    (D)  TOPOLOGY: linear

(ii)  MOLECULE TYPE: protein




(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
        115             120             125

Ile Ser Thr Ile Asn Pro Ser Pro Ser Lys Glu Ser His Lys Ser
    130             135             140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
145             150             155             160

Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
            165             170             175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
        180             185             190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
        195             200             205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
    210             215             220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
225             230             235             240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
            245             250             255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu


                                 135
```

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
        275   280   285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
    290   295   300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
305   310   315   320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:131:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 259 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20   25   30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35   40   45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
        115   120   125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130   135   140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145   150   155   160

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
            165   170   175

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
            180   185   190

Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
            195   200   205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
    210   215   220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225   230   235   240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
            245   250   255

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:132:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 259 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

     Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
     1   5   10   15

     Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                 20   25   30

     Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
                 35   40   45

     Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
                 50   55   60

     Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
     65   70   75   80

     Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                 85   90   95

     Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                 100   105   110

     Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro
                 115   120   125

     Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
                 130   135   140

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Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145   150   155   160

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
                165   170   175

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
            180   185   190

Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
            195   200   205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
    210   215   220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225   230   235   240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
            245   250   255

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:133:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 259 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

    Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
    1   5   10   15

    Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                20   25   30

    Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
            35   40   45

    Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

    Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
    65   70   75   80

    Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

    Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                100   105   110

    Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro

138

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130   135   140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145   150   155   160

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
                165   170   175

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
                180   185   190

Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
                195   200   205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
    210   215   220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225   230   235   240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
                245   250   255

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:134:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 307 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
                20   25   30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
                35   40   45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
        100   105   110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115   120   125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
130   135   140

Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145   150   155   160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
            165   170   175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
            180   185   190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
            195   200   205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
    210   215   220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225   230   235   240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
            245   250   255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
            260   265   270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
    275   280   285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
    290   295   300

Ala Gln Pro
305

(2) INFORMATION FOR SEQ ID NO:135:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

    Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
    1   5   10   15

```
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20              25              30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115             120             125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
    130             135             140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145             150             155             160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
                165             170             175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
            180             185             190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
        195             200             205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
210             215             220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225             230             235             240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
            245             250             255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
        260             265             270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
        275             280             285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
290             295             300

Ala Gln Pro
305
```

(2) INFORMATION FOR SEQ ID NO:136:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 amino acids

(B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

    Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
    1   5   10   15

    Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
                20   25   30

    Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
                35   40   45

    Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
            50   55   60

    Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
    65   70   75   80

    Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                    85   90   95

    Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                100   105   110

    Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
            115   120   125

    Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
        130   135   140

    His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
    145   150   155   160

    Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
                    165   170   175

    Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
                180   185   190

    Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
            195   200   205

    Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
        210   215   220

    Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
    225   230   235   240

    Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:137:

142

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 259 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                  15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20              25                  30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40                  45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70              75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105                 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
        115             120                 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130             135                 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145             150                 155                 160

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
            165                 170                 175

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
            180                 185                 190

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
        195                 200                 205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
    210                 215                 220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225             230                 235                 240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
            245                 250                 255
```

143

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:138:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 322 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                  15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20                  25                  30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35                  40                  45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50                  55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85                  90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100                 105                 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
        115                 120                 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130                 135                 140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
145                 150                 155                 160

Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
            165                 170                 175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
            180                 185                 190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
        195                 200                 205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
    210                 215                 220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
```

144

```
      225                 230                 235                 240
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
                245                 250                 255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
                260                 265                 270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
                275                 280                 285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
                290                 295                 300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
305                 310                 315                 320

Gln Pro
```

(2) INFORMATION FOR SEQ ID NO:139:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 349 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
            35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala
            115             120             125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
            130             135             140
```

145

```
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
145             150             155             160

Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Thr
            165             170             175

Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser
            180             185             190

Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
            195             200             205

Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
210             215             220

Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
225             230             235             240

Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
            245             250             255

Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
            260             265             270

Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
            275             280             285

Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala
            290             295             300

Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
305             310             315             320

Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
            325             330             335

Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            340             345
```

(2) INFORMATION FOR SEQ ID NO:140:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
GGATCCACCA TGAGCCGCCT GCCCGTCCTG CTCCTGCTCC AACTCCTGGT CCGCCCCGCC      60

ATGG      64
```

(2) INFORMATION FOR SEQ ID NO:141:

```
(i)  SEQUENCE CHARACTERISTICS:
     (A)  LENGTH: 259 amino acids
     (B)  TYPE: amino acid
     (C)  STRANDEDNESS:
     (D)  TOPOLOGY: linear

(ii) MOLECULE TYPE: protein




(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5                   10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20                  25                  30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35                  40                  45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50                  55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85                  90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100                 105                 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Asn Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro
    130                 135                 140

Trp Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu
145                 150                 155                 160

Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser
            165                 170                 175

Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu
            180                 185                 190

Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
        195                 200                 205

Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro
    210                 215                 220

Glu Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu
225                 230                 235                 240

Asn Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro
            245                 250                 255
```

147

Val Gln Glu

(2) INFORMATION FOR SEQ ID NO:142:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 301 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20   25   30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35   40   45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala
        115   120   125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
        130   135   140

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
145   150   155   160

Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Pro
            165   170   175

Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala
            180   185   190

Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala
        195   200   205

Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln
        210   215   220

148

```
Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln Gly Leu
225                 230                 235                 240

Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met Ala Ser
                245                 250                 255

His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys Ala Thr
            260                 265                 270

Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
            275                 280                 285

Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:143:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 335 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10                  15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25                  30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
            35              40                  45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                100                 105                 110

Gln Tyr Val Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly
            115                 120                 125

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly
        130                 135                 140

Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asn Met
145                 150                 155                 160

Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
```

<div align="center">149</div>

```
                        165                    170                    175
    Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
                    180                    185                    190
    Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
                    195                    200                    205
    Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
                210                    215                    220
    Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
    225                    230                    235                    240
    Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                    245                    250                    255
    Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
                    260                    265                    270
    Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
                    275                    280                    285
    Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
                290                    295                    300
    Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
    305                    310                    315                    320
    Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                    325                    330                    335
```

(2) INFORMATION FOR SEQ ID NO:144:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 274 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
    Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
    1                   5                   10                  15
    Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                    20                  25                  30
    Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
                35                  40                  45
    Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
                50                  55                  60
    Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
    65                  70                  75                  80
```

```
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85              90                      95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
        115             120             125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130             135             140

Pro Asn Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp
145             150             155                     160

Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser
            165             170             175

Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu
            180             185             190

Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu
        195             200             205

Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu
    210             215             220

Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu
225             230             235                     240

Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn
            245             250             255

Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val
            260             265             270

Gln Glu
```

(2) INFORMATION FOR SEQ ID NO:145:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 317 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30
```

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35   40   45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115   120   125

Gly Ser Asn Met Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val
    130   135   140

Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys
145   150   155   160

Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr
                165   170   175

Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu
            180   185   190

Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln
        195   200   205

Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu
    210   215   220

Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
225   230   235   240

Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile
            245   250   255

Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
        260   265   270

Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
    275   280   285

Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys
    290   295   300

Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
305   310   315

(2) INFORMATION FOR SEQ ID NO:146:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

152

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1               5               10              15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20              25              30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35              40              45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
    50              55              60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65              70              75              80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85              90              95          .

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100             105             110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115             120             125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130             135             140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145             150             155             160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            165             170             175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
            180             185             190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
            195             200             205

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
    210             215             220

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
225             230             235             240

Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
            245             250             255

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
            260             265             270

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
    275             280             285
```

153

```
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
    290                 295                 300

Glu Gln Gln
305
```

(2) INFORMATION FOR SEQ ID NO:147:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1               5               10                  15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20              25              30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
            35              40              45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
            50              55              60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65                  70              75                  80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85              90                  95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100             105             110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
            115             120             125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
    130             135             140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145             150             155             160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            165             170             175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
            180             185             190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
    195             200             205
```

154

```
Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
    210             215             220
```

```
Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
225             230             235                     240
```

```
Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
                245             250                     255
```

```
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
            260             265             270
```

```
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
        275             280             285
```

```
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
    290             295             300
```

```
Glu Gln Gln
305
```

(2)   INFORMATION FOR SEQ ID NO:148:

   (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 337 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS:
        (D)   TOPOLOGY: linear

   (ii)   MOLECULE TYPE: protein

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1               5               10                      15
```

```
Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20              25              30
```

```
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
            35              40              45
```

```
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
        50              55              60
```

```
Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65              70              75                      80
```

```
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
            85              90                      95
```

```
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100             105             110
```

```
Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115             120             125
```

```
Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
```

```
              130                    135                    140
Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145                150                155                    160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                 165                170                175

Tyr Val Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly
             180                185                190

Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
             195                200                205

Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly
             210                215                220

Asp Phe Asp Tyr Glu Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu
225                230                235                    240

Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn
                 245                250                255

Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg
             260                265                270

Leu Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
             275                280                285

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
             290                295                300

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
305                310                315                    320

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                 325                330                335

Gln
```

(2) INFORMATION FOR SEQ ID NO:149:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 322 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1                5                 10                15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
             20                25                30
```

```
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35                  40                  45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
        50                  55                  60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65                  70                  75                      80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85                  90                  95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100                 105                 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
            115                 120                 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130                 135                 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145                 150                 155                     160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
            180                 185                 190

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
            195                 200                 205

Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
    210                 215                 220

Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
225                 230                 235                     240

Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
                245                 250                 255

Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
                260                 265                 270

Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
            275                 280                 285

Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
    290                 295                 300

Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
305                 310                 315                     320

Gln Gln
```

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1   5   10   15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20   25   30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
            35   40   45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
        50   55   60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65   70   75   80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85   90   95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100   105   110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
            115   120   125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130   135   140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145   150   155   160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165   170   175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
            180   185   190

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
            195   200   205

Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
    210   215   220

Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
225   230   235   240

Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu
                245   250   255

Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu

                             158

Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
        275   280   285

Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
    290   295   300

Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
305   310   315   320

Gln Gln

(2) INFORMATION FOR SEQ ID NO:151:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 349 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1   5   10   15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20   25   30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35   40   45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
    50   55   60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65   70   75   80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
            85   90   95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100   105   110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115   120   125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
    130   135   140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145   150   155   160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            165   170   175

159

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala Gly
            180   185   190

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser
            195   200   205

Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly
    210   215   220

Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Asn Cys
225   230   235   240

Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn
            245   250   255

Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu
            260   265   270

Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala
            275   280   285

Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
    290   295   300

Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
305   310   315   320

Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
            325   330   335

Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
            340   345

(2) INFORMATION FOR SEQ ID NO:152:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 307 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

     Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
     1   5   10   15

     Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
                 20   25   30

     Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
                 35   40   45

     Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
         50   55   60

160

```
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65                  70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85                  90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                100                 105                 110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
            115                 120                 125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
        130                 135                 140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145                 150                 155                 160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
                165                 170                 175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
                180                 185                 190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
            195                 200                 205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
    210                 215                 220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225                 230                 235                 240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
            245                 250                 255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
            260                 265                 270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
            275                 280                 285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
    290                 295                 300

Ala Gln Pro
305
```

(2) INFORMATION FOR SEQ ID NO:153:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20              25              30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
        115             120             125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
    130             135             140

His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
145             150             155             160

Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
            165             170             175

Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
        180             185             190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
    195             200             205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
    210             215             220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225             230             235             240

Gln Glu Gln Gln
```

(2) INFORMATION FOR SEQ ID NO:154:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 322 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
                20              25              30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35              40              45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
        115             120             125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
    130             135             140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
145             150             155             160

Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
            165             170             175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
        180             185             190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
        195             200             205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
    210             215             220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
225             230             235             240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
            245             250             255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
            260             265             270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
        275             280             285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
    290             295             300
```

163

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
305   310   315   320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:155:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 259 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1   5   10   15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20   25   30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
            35   40   45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
    50   55   60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65   70   75   80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                85   90   95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100   105   110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
        115   120   125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
        130   135   140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145   150   155   160

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
            165   170   175

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
            180   185   190

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
        195   200   205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala

164

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225   230   235   240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
                245   250   255

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:156:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 322 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1   5   10   15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20   25   30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35   40   45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
        50   55   60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
65   70   75   80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85   90   95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100   105   110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115   120   125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130   135   140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145   150   155   160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165   170   175

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile
            180   185   190

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
195 200 205

Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
210 215 220

Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
225 230 235 240

Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
245 250 255

Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
260 265 270

Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
275 280 285

Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
290 295 300

Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
305 310 315 320

Gln Gln

(2) INFORMATION FOR SEQ ID NO:157:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 322 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

    Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
    1   5   10   15

    Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
                 20   25   30

    Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
                 35   40   45

    Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
                 50   55   60

    Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
    65   70   75   80

    His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                 85   90   95

```
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
        100                 105                 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115                 120                 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130                 135                 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145                 150                 155                 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile
                180                 185                 190

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
        195                 200                 205

Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
        210                 215                 220

Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
225                 230                 235                 240

Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
                245                 250                 255

Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
                260                 265                 270

Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
        275                 280                 285

Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
        290                 295                 300

Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
305                 310                 315                 320

Gln Gln
```

(2) INFORMATION FOR SEQ ID NO:158:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

   Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu

167

```
              1                 5                      10                      15
              Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
                        20                  25                  30

              Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
                        35              40                  45

              Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
                        50              55                  60

              Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
              65                  70                  75                      80

              His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                                85                  90                  95

              Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
                            100                 105                 110

              Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
                            115                 120                 125

              Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
                            130                 135                 140

              Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
              145                 150                 155                 160

              Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                                165                 170                 175

              Tyr Val Glu Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly
                            180                 185                 190

              Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
                            195                 200                 205

              Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
                            210                 215                 220

              Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
              225                 230                 235                 240

              Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
                            245                 250                 255

              Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
                            260                 265                 270

              Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
                            275                 280                 285

              Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
                            290                 295                 300

              Glu Gln Gln
              305

(2)  INFORMATION FOR SEQ ID NO:159:
```

168

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 307 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1               5                   10                  15

Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20                  25                  30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35                  40                  45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
    50                  55                  60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
65                  70                  75                  80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85                  90                  95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100                 105                 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115                 120                 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130                 135                 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145                 150                 155                 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly
                180                 185                 190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
            195                 200                 205

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
        210                 215                 220

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
225                 230                 235                 240

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
                245                 250                 255
```

169

```
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
            260                 265                 270

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
            275                 280                 285

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
290                 295                 300

Glu Gln Gln
305
```

(2) INFORMATION FOR SEQ ID NO:160:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
1               5                   10                  15

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
            20                  25                  30

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
            35                  40                  45

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
    50                  55                  60

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
65                  70                  75                  80

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
                85                  90                  95

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
            100                 105                 110

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
            115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:161:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 176 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1               5                   10                  15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20                  25                  30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35                  40                  45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
    50                  55                  60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65                  70                  75                  80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
            85                  90                  95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
            100                 105                 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
        115                 120                 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
    130                 135                 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145                 150                 155                 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:162:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 176 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

                                            .

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1               5                   10                  15

Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
            20                  25                  30
```

```
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
        35                  40                  45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
        50                  55                  60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65                  70                  75                      80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
                85                  90                  95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
                100                 105                 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
            115                 120                 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
        130                 135                 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145                 150                 155                     160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:163:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 186 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
Met Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro
1               5                   10                  15

His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg
                20                  25                  30

Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys
            35                  40                  45

Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu
        50                  55                  60

Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe
65                  70                  75                      80

Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe
                85                  90                  95
```

172

Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu
        100   105   110

Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu
        115   120   125

Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr
    130   135   140

Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu
145   150   155   160

Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu
                165   170   175

Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
            180   185

(2) INFORMATION FOR SEQ ID NO:164:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 155 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1   5   10   15

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
            20   25   30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe
            35   40   45

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp
    50   55   60

Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
65   70   75   80

Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser
                85   90   95

Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
            100   105   110

Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
        115   120   125

Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
    130   135   140

Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg

(2) INFORMATION FOR SEQ ID NO:165:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 286 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1               5               10              15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
            20              25              30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
        35              40              45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
        50              55              60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65              70              75              80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
            85              90              95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
            100             105             110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
        115             120             125

Gly Ser Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
    130             135             140

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
145             150             155             160

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
            165             170             175

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
        180             185             190

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
        195             200             205

Ala Ala Arg Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
    210             215             220

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
225             230             235             240
```

```
              Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
                          245             250             255

              Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
                          260             265             270

              Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg
                          275             280             285
```

(2) INFORMATION FOR SEQ ID NO:166:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 286 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
              Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
              1               5               10              15

              Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
                          20              25              30

              Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
                          35              40              45

              Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
                          50              55              60

              Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
              65              70              75              80

              Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
                          85              90              95

              Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
                          100             105             110

              Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
                          115             120             125

              Gly Ser Asn Met Ala Ser Pro Ala Pro Ala Cys Asp Leu Arg Val
                          130             135             140

              Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
              145             150             155             160

              Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
                          165             170             175

              Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
                          180             185             190
```

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
    195   200   205

Ala Ala Arg Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
    210   215   220

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
225   230   235   240

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
                245   250   255

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
            260   265   270

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg
        275   280   285

(2) INFORMATION FOR SEQ ID NO:167:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 286 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1   5   10   15

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
            20   25   30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe
            35   40   45

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp
    50   55   60

Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
65   70   75   80

Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser
                85   90   95

Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
            100   105   110

Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
        115   120   125

Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
    130   135   140

Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Tyr Val Ile Glu Gly

176

Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Asn
                    165   170   175

Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro
            180   185   190

Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile
        195   200   205

Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg
    210   215   220

Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
225   230   235   240

Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His
            245   250   255

Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu
            260   265   270

Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
            275   280   285

(2) INFORMATION FOR SEQ ID NO:168:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 290 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1   5   10   15

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
                20   25   30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe
            35   40   45

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp
    50   55   60

Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
65   70   75   80

Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser
                85   90   95

Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
                100   105   110

```
Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
        115             120             125

Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
        130             135             140

Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe His Ala Tyr
145             150             155             160

Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser
            165             170             175

Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
        180             185             190

Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
        195             200             205

Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu
210             215             220

Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu
225             230             235             240

Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
            245             250             255

Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
            260             265             270

Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
            275             280             285

Gln Gln
290
```

(2) INFORMATION FOR SEQ ID NO:169:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACGTCCATGG CNTCNCCNGC NCCNCCTGCT TGTGACCTCC GAGTC   45

(2) INFORMATION FOR SEQ ID NO:170:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

AATAGCTGAA TTCTTACCCT TCCTGAGACA GATT   34

(2) INFORMATION FOR SEQ ID NO:171:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 33 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGACAAGCTT ACCTGACGCA GAGGGTGGAC CCT   33

(2) INFORMATION FOR SEQ ID NO:172:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ATGCACGAAT TCCCTGACGC AGAGGGTGGA   30

(2) INFORMATION FOR SEQ ID NO:173:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

AATTCCATGC ATAC   14

(2) INFORMATION FOR SEQ ID NO:174:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 10 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: other nucleic acid
  (A) DESCRIPTION: /desc = "synthetic DNA"

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTACGTATG   10

(2) INFORMATION FOR SEQ ID NO:175:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 561 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: DNA (genomic)

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

ATGGCTCCAG TACCACCAGG TGAAGATTCC AAAGATGTGG CCGCCCCACA CAGACAGCCA   60

CTCACCTCTT CAGAACGAAT TGACAAACAA ATTCGGTACA TCCTCGACGG GATATCAGCC   120

CTGAGAAAGG AGACATGTAA CAAGAGTAAC ATGTGTGAAA GCAGCAAAGA GGCGCTAGCA   180

GAAAACAACC TGAACCTTCC AAAGATGGCT GAAAAAGATG GATGCTTCCA ATCCGGATTC   240

AATGAGGAGA CTTGCCTGGT GAAAATCATC ACTGGTCTTT TGGAGTTTGA GGTATACCTC   300

GAGTACCTCC AGAACAGATT TGAGAGTAGT GAGGAACAAG CCAGAGCTGT GCAGATGTCG   360

ACAAAAGTCC TGATCCAGTT CCTGCAGAAA AAGGCAAAGA ATCTAGATGC AATAACCACC   420

CCTGACCCAA CCACAAATGC ATCCCTGCTG ACGAAGCTGC AGGCACAGAA CCAGTGGCTG   480

CAGGACATGA CAACTCATCT CATTCTGCGC AGCTTTAAGG AGTTCCTGCA GTCCAGCCTG   540

AGGGCTCTTC GGCAAATGTA G   561

(2) INFORMATION FOR SEQ ID NO:176:

 (i) SEQUENCE CHARACTERISTICS:

180

```
        (A)  LENGTH: 402 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: double
        (D)  TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)




    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ATGGCACCGG CTCGTTCCCC GTCCCCGTCT ACCCAGCCGT GGGAACACGT GAATGCCATC        60

CAGGAGGCCC GGCGTCTCCT GAACCTGAGT AGAGACACTG CTGCTGAGAT GAATGAAACA       120

GTAGAAGTGA TATCAGAAAT GTTTGACCTC CAGGAGCCGA CTTGCCTACA GACCCGCCTG       180

GAGCTGTACA AGCAGGGCCT GCGGGGCAGC CTCACCAAGC TCAAGGGCCC CTTGACCATG       240

ATGGCCAGCC ACTACAAGCA GCACTGCCCT CCAACCCCGG AAACTTCCTG TGCAACCCAG       300

ATTATCACCT TTGAAAGTTT CAAAGAGAAC CTGAAGGACT TCCTGCTTGT CATCCCCTTT       360

GACTGCTGGG AGCCAGTCCA GGAGTGATAA GGATCCGAAT TC                         402
```

(2) INFORMATION FOR SEQ ID NO:177:

```
        (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 546 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: double
            (D)  TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)




    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA        60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC       120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG       180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC       240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG       300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG       360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG       420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG       480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC       540

GAATTC                                                                 546
```

(2) INFORMATION FOR SEQ ID NO:178:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 546 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
ATGGCTACAC CATTAGGACC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA      60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC     120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG     180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC     240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG     300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG     360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG     420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG     480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC     540

GAATTC                                                              546
```

(2) INFORMATION FOR SEQ ID NO:179:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 546 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA      60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC     120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG     180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC     240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG     300

TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG     360
```

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG   420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG   480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC   540

GAATTC   546

(2) INFORMATION FOR SEQ ID NO:180:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 465 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC   60

TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT   120

GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC   180

AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG   240

GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT   300

CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC   360

ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG   420

GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGG   465

(2) INFORMATION FOR SEQ ID NO:181:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 143 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCTGTCAACC CGGGCGGCGG CTCTGGTGGT GGTTCTGGTG GCGGCTCTGA GGGTGGCGGC   60

TCTGAGGGTG GCGGTTCTGA GGGTGGCGGC TCTGAGGGTG GCGGTTCCGG TGGCGGCTCC   120

GGTTCCGGTA ACATGTATTA TGA   143

(2) INFORMATION FOR SEQ ID NO:182:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 180 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```
ATCGTCTGAC CTCCCGGGCC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT        60

GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT       120

GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTTGATT ATGAAAACAT GTCAAACGCT       180
```

(2) INFORMATION FOR SEQ ID NO:183:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 858 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC        60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC       120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA       180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC       240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG       300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT       360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCGT CTCCGGCGCC GCCTGCTTGT       420

GACCTCCGAG TCCTCAGTAA ACTGCTTCGT GACTCCCATG TCCTTCACAG CAGACTGAGC       480

CAGTGCCCAG AGGTTCACCC TTTGCCTACA CCTGTCCTGC TGCCTGCTGT GGACTTTAGC       540

TTGGGAGAAT GGAAAACCCA GATGGAGGAG ACCAAGGCAC AGGACATTCT GGGAGCAGTG       600

ACCCTTCTGC TGGAGGGAGT GATGGCAGCA CGGGGACAAC TGGGACCCAC TTGCCTCTCA       660

TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC       720
```

CTTGGAACCC AGCTTCCTCC ACAGGGCAGG ACCACAGCTC ACAAGGATCC CAATGCCATC   780

TTCCTGAGCT TCCAACACCT GCTCCGAGGA AAGGTGCGTT TCCTGATGCT TGTAGGAGGG   840

TCCACCCTCT GCGTCAGG   858

    (2) INFORMATION FOR SEQ ID NO:184:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 858 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC   60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC   120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA   180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCGT CTCCGGCGCC GCCTGCTTGT   420

GACCTCCGAG TCCTCAGTAA ACTGCTTCGT GACTCCCATG TCCTTCACAG CAGACTGAGC   480

CAGTGCCCAG AGGTTCACCC TTTGCCTACA CCTGTCCTGC TGCCTGCTGT GGACTTTAGC   540

TTGGGAGAAT GGAAAACCCA GATGGAGGAG ACCAAGGCAC AGGACATTCT GGGAGCAGTG   600

ACCCTTCTGC TGGAGGGAGT GATGGCAGCA CGGGGACAAC TGGGACCCAC TTGCCTCTCA   660

TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC   720

CTTGGAACCC AGCTTCCTCC ACAGGGCAGG ACCACAGCTC ACAAGGATCC CAATGCCATC   780

TTCCTGAGCT TCCAACACCT GCTCCGAGGA AAGGTGCGTT TCCTGATGCT TGTAGGAGGG   840

TCCACCCTCT GCGTCAGG   858

    (2) INFORMATION FOR SEQ ID NO:185:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 852 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```
ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC          60

TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT         120

GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC         180

AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG         240

GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT         300

CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC         360

ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG         420

GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGATCGA GGGAAGGATT         480

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT         540

GAAATTATAC ATCACTTAAA GAGACCACCT AACCCTTTGC TGGACCCGAA CAACCTCAAT         600

TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC         660

GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC         720

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA         780

GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG         840

CAGGAACAAC AG                                                            852
```

(2) INFORMATION FOR SEQ ID NO:186:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 870 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC          60

TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT         120

GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC         180

AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG         240

GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT         300

CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC         360
```

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```
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG    420

GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CCATGCATAC    480

GTAGAGGGCG GTGGAGGCTC CCCGGGTGGT GGTTCTGGCG GCGGCTCCAA CATGGCTAAC    540

TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTAA CCCTTTGCTG    600

GACCCGAACA ACCTCAATTC TGAAGACATG GATATCCTGA TGGAACGAAA CCTTCGAACT    660

CCAAACCTGC TCGCATTCGT AAGGGCTGTC AAGCACTTAG AAAATGCATC AGGTATTGAG    720

GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT    780

CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAACTGAC GTTCTATCTG    840

GTTACCCTTG AGCAAGCGCA GGAACAACAG                                     870
```

(2) INFORMATION FOR SEQ ID NO:187:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```
Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
1               5                   10                  15

Ala Met
```

(2) INFORMATION FOR SEQ ID NO:188:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```
Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
1               5                   10                  15

Ser Asn
```

(2) INFORMATION FOR SEQ ID NO:189:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 18 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS:
               (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: peptide

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

         Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
         1   5   10   15

         Ser Asn

(2) INFORMATION FOR SEQ ID NO:190:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 18 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS:
               (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: peptide

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

         Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly
         1   5   10   15

         Ser Asn

(2) INFORMATION FOR SEQ ID NO:191:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 33 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS:
               (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: peptide

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

         Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
         1   5   10   15

         Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro

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Asn

(2) INFORMATION FOR SEQ ID NO:192:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
1   5   10   15

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
                20   25   30

Asn

(2) INFORMATION FOR SEQ ID NO:193:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile
1   5   10   15

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
                20   25   30

Asn

(2) INFORMATION FOR SEQ ID NO:194:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 49 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
1               5               10              15

Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
            20              25              30

Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly
        35              40              45

Asn
```


(2) INFORMATION FOR SEQ ID NO:195:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala Gly
1               5               10              15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser
            20              25              30

Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly
        35              40              45

Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn
    50              55              60
```

(2) INFORMATION FOR SEQ ID NO:196:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```
Glu Phe His Ala Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly
1               5               10              15

Ser Gly Gly Gly Ser Asn
                20
```

(2) INFORMATION FOR SEQ ID NO:197:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 408 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA other nucleic acid
        (A) DESCRIPTION: /desc = "synthetic DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

```
ATGGCTCCAA TGACTCAGAC TACTTCTCTT AAGACTTCTT GGGTTAACTG CTCTAACATG    60

ATCGATGAAA TTATAACACA CTTAAAGCAG CCACCTTTGC CTTTGCTGGA CTTCAACAAC   120

CTCAATGGGG AAGACCAAGA CATTCTGATG GAAAATAACC TTCGAAGGCC AAACCTGGAG   180

GCATTCAACA GGGCTGTCAA GAGTTTACAG AATGCATCAG CAATTGAGAG CATTCTTAAA   240

AATCTCCTGC CATGTCTGCC CCTGGCCACG GCCGCACCCA CGCGACATCC AATCCATATC   300

AAGGACGGTG ACTGGAATGA ATTCCGTCGT AAACTGACCT TCTATCTGAA AACCTTGGAG   360

AACGCGCAGG CTCAACAGAC CACTCTGTCG CTAGCGATCT TTTAATAA              408
```

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